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XX W0200121188-A1.
XX 29-MAR-2001.
XX 22-SEP-1999; 99WO-US21770.
XX 22-SEP-1999; 99WO-US21770.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX WPI; 2001-211457/21.
XX New serum amyloid A and formyl peptide receptor variant complex and its
XX modulators, useful for treating immune system disorders, amyloidosis,
XX inflammation, infection, organ rejection, arthritis, atherosclerosis
XX and neoplasia -
XX
XX Disclosure; Page 16; 141pp; English.
XX The present sequence is a fragment of human serum amyloid A (SAA). The
XX invention relates to the discovery that SAA is a ligand for FPR1 (human
XX formyl peptide receptor variant). A complex has been isolated that
XX comprises a peptide agent with a sequence corresponding to SAA, or its
XX conservative variant or functional fragment, bound to FPR1. Modulators
XX of the SAA/FPR1 complex are useful for treating immune system
XX disorders, amyloidosis, inflammation, infection, organ rejection,
XX arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
XX for their ability to modulate assembly of the SAA/FPR1 complex.
XX
SQ Sequence 55 AA:
Query Match 100.0%; Score 23; DB 22; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
YY 1 NYDA 4
DB 42 NYDA 45
RESULT 32
AAB90296
ID AAB90296 standard; Protein; 56 AA.
XX
XX AAB90296;
XX 01-JUN-2001 (first entry)
XX Human SAA carboxy truncation, SEQ ID NO: 54.
XX
XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;
XX FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
XX antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
XX immune system disorder; amyloidosis; inflammation; infection;
XX organ rejection; arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX W0200121188-A1.
XX 29-MAR-2001.
XX 22-SEP-1999; 99WO-US21770.
XX 22-SEP-1999; 99WO-US21770.
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XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
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DR WPI; 2001-211457/21.
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XX invention relates to the discovery that SAA is a ligand for FPR1 (human
XX formyl peptide receptor variant). A complex has been isolated that
XX comprises a peptide agent with a sequence corresponding to SAA, or its
XX conservative variant or functional fragment, bound to FPR1. Modulators
XX of the SAA/FPR1 complex are useful for treating immune system
XX disorders, amyloidosis, inflammation, infection, organ rejection,
XX arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
XX for their ability to modulate assembly of the SAA/FPR1 complex.
XX
SQ Sequence 56 AA:
Query Match 100.0%; Score 23; DB 22; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
YY 1 NYDA 4
DB 42 NYDA 45
RESULT 33
AAB90297
ID AAB90297 standard; Protein; 57 AA.
XX
XX AAB90297;
XX 01-JUN-2001 (first entry)
XX Human SAA carboxy truncation, SEQ ID NO: 55.
XX
XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;
XX FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
XX antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
XX immune system disorder; amyloidosis; inflammation; infection;
XX organ rejection; arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX W0200121188-A1.
XX 29-MAR-2001.
XX 22-SEP-1999; 99WO-US21770.
XX 22-SEP-1999; 99WO-US21770.
XX 22-SEP-1999; 99WO-US21770.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
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XX modulators, useful for treating immune system disorders, amyloidosis,
XX inflammation, infection, organ rejection, arthritis, atherosclerosis
XX and neoplasia -
XX
XX Disclosure; Page 16; 141pp; English.
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XX invention relates to the discovery that SAA is a ligand for FPR1 (human
XX formyl peptide receptor variant). A complex has been isolated that
XX comprises a peptide agent with a sequence corresponding to SAA, or its

CC conservative variant or functional fragment, bound to FPR1. Modulators
 CC of the SAA/FPRL1 complex are useful for treating immune system
 CC disorders, amyloidosis, inflammation, infection, organ rejection,
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.

XX Sequence 57 AA;

Query Match 100.0%; Score 23; DB 22; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2,2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 42 NYDA 45

RESULT 34

AA678507 standard; protein; 58 AA.

XX AAG78507;

XX 15-JAN-2002 (first entry)

DE Mouse serum amyloid A protein N-terminal fragment.

XX Amyloid; Amyloidosis; Amyloid fibril; Serum amyloid A protein;
 XX Nootropic; Neuroprotective; Cytostatic; Cerebroprotective;
 KM Cardiac; Anti diabetic; Anti inflammatory; Alzheimer's disease;
 KM Multiple myeloma; Neuropathy; Cardiomypathy; Adult onset diabetes;
 KM Monoclonal plasma cell dyscrasia; Inflammation; Aging; Scrapie;
 KM Bovine spongiform encephalopathy; BSE; Creutzfeldt-Jacob disease; CJD;
 KM Familial Mediterranean fever.

XX hms sp.

XX WO200177167-A2.

PD 18-OCT-2001.

PF 05-APR-2001; 2001WO-US11043.

PR 05-APR-2000; 2000US-194684P.

PA (UYTE-) UNIV TENNESSEE RES CORP.

XX Solomon A, Wall J, Hincic R, Schell M;

DR WPI; 2001-663054/76.

PT Removing amyloid deposits from patient used for treating e.g.
 PT Alzheimer's disease comprises administering amyloid fibril -

XX Disclosure; Fig 3; 57pp; English.

XX The invention relates to a method for the removal of amyloid deposits
 CC from a patient comprising administering an amyloid fibril to generate an
 CC immune response that promotes in vivo removal of the amyloid fibrils.
 CC The methods of this invention are useful for the removal of amyloid
 CC deposits from a patient. Other uses include the investigation of AA
 CC amyloidosis with a transgenic animal and the evaluating of agents that
 CC may be potentially useful in preventing and treating amyloid-related
 CC disorders. They may be used for diagnostic assays for monitoring
 CC immunoglobulin light chain fibrillogenesis and for identification of the
 CC chemical nature of the protein in amyloid deposits that enables the
 CC determination of the type of amyloidosis for therapeutic and prognostic
 CC applications e.g. in treating Alzheimer's disease, multiple myeloma,
 CC neuropathies, cardiomyopathies, monoclonal plasma cell dyscrasias, adult
 CC onset diabetes, chronic inflammation, aging, bovine spongiform
 CC encephalopathy, Creutzfeldt-Jacob disease and scrapie. AA amyloid is
 CC also commonly found in various forms of malignancy and in Familial
 CC Mediterranean fever. The method provides a useful and stable transgenic

CC animal model for investigating AA amyloidosis. The current sequence
 CC represents residues 1-58 of a mouse serum amyloid A amino acid sequence.

XX Sequence 58 AA;

Query Match 100.0%; Score 23; DB 22; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 40 NYDA 43

RESULT 35

AA690298 standard; protein; 58 AA.

XX AAB90298;

XX 01-JUN-2001 (first entry)

DE Human SAA carboxy truncation, SEQ ID NO: 56.

XX Human; serum amyloid A; SAA; human; formyl peptide receptor variant;
 KM FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
 KM antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;
 KM immune system disorder; amyloidosis; inflammation; infection;
 KM organ rejection; arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200121188-A1.

PD 29-MAR-2001.

PF 22-SEP-1999; 99WO-US21770.

PR 22-SEP-1999; 99WO-US21770.

PA (USSR) US DEPT HEALTH & HUMAN SERVICES.

XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

DR WPI; 2001-211457/21.

PT New serum amyloid A and formyl peptide receptor variant complex and its
 PT modulators, useful for treating immune system disorders, amyloidosis,
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis
 PT and neoplasia -

XX Disclosure; Page 16; 14pp; English.

XX The present sequence is a fragment of human serum amyloid A (SAA). The
 CC invention relates to the discovery that SAA is a ligand for FPR1 (human
 CC formyl peptide receptor variant). A complex has been isolated that
 CC comprises a peptide agent with a sequence corresponding to SAA, or its
 CC conservative variant or functional fragment, bound to FPR1. Modulators
 CC of the SAA/FPRL1 complex are useful for treating immune system
 CC disorders, amyloidosis, inflammation, infection, organ rejection,
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.

XX Sequence 58 AA;

Query Match 100.0%; Score 23; DB 22; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 42 NYDA 45

RESULT 36
AAB90299
ID AAB90299 standard; Protein: 59 AA.
XX
XX AAB90299;
XX
XX 01-JUN-2001 (first entry)
XX
XX Human SAA carboxy truncation, SEQ ID NO: 57.
XX
XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;
XX
XX FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
XX
XX antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
XX
XX immune system disorder; amyloidosis; inflammation; infection;
XX
XX organ rejection; arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200121188-A1.
XX
XX 29-MAR-2001.
XX
XX 22-SEP-1999; 99WO-US21770.
XX
XX 22-SEP-1999; 99WO-US21770.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
XX WPI; 2001-211457/21.
XX
XX New serum amyloid A and formyl peptide receptor variant complex and its
XX
XX modulators, useful for treating immune system disorders, amyloidosis,
XX
XX inflammation, infection, organ rejection, arthritis, atherosclerosis
XX
XX and neoplasia -
XX
XX Disclosure; Page 16; 141pp; English.
XX
XX The present sequence is a fragment of human serum amyloid A (SAA). The
XX
XX invention relates to the discovery that SAA is a ligand for FPR1 (human
XX
XX formyl peptide receptor variant). A complex has been isolated that
XX
XX comprises a peptide agent with a sequence corresponding to SAA, or its
XX
XX conservative variant or functional fragment, bound to FPR1. Modulators
XX
XX of the SAA/FPR1 complex are useful for treating immune system
XX
XX disorders, amyloidosis, inflammation, infection, organ rejection,
XX
XX arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
XX
XX for their ability to modulate assembly of the SAA/FPR1 complex.
XX
XX Sequence 59 AA:
XX
XX Query Match 100.0%; Score 23; DB 22; Length 59;
XX
XX Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
XX
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYDA 4
DB 42 NYDA 45

RESULT 37
AAB90300
ID AAB90300 standard; Protein: 60 AA.
XX
XX AAB90300;
XX
XX 01-JUN-2001 (first entry)
XX
XX Human SAA carboxy truncation, SEQ ID NO: 58.
XX
XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;
XX
XX FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
XX
XX

KW antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200121188-A1.
XX
XX 29-MAR-2001.
XX
XX 22-SEP-1999; 99WO-US21770.
XX
XX 22-SEP-1999; 99WO-US21770.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
XX WPI; 2001-211457/21.
XX
XX New serum amyloid A and formyl peptide receptor variant complex and its
XX
XX modulators, useful for treating immune system disorders, amyloidosis,
XX
XX inflammation, infection, organ rejection, arthritis, atherosclerosis
XX
XX and neoplasia -
XX
XX Disclosure; Page 16; 141pp; English.
XX
XX The present sequence is a fragment of human serum amyloid A (SAA). The
XX
XX invention relates to the discovery that SAA is a ligand for FPR1 (human
XX
XX formyl peptide receptor variant). A complex has been isolated that
XX
XX comprises a peptide agent with a sequence corresponding to SAA, or its
XX
XX conservative variant or functional fragment, bound to FPR1. Modulators
XX
XX of the SAA/FPR1 complex are useful for treating immune system
XX
XX disorders, amyloidosis, inflammation, infection, organ rejection,
XX
XX arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
XX
XX for their ability to modulate assembly of the SAA/FPR1 complex.
XX
XX Sequence 60 AA:
XX
XX Query Match 100.0%; Score 23; DB 22; Length 60;
XX
XX Best Local Similarity 100.0%; Pred. NO. 2.4e+02;
XX
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYDA 4
DB 42 NYDA 45

RESULT 38
ABP09824
ID ABP09824 standard; Protein: 60 AA.
XX
XX ABP09824;
XX
XX 24-JUN-2002 (first entry)
XX
XX Human ORFX protein sequence SEQ ID NO:19630.
XX
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX
XX hyperproliferative disorder; psoriasis; benign tumour; hemorrhage;
XX
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX
XX hypertension; hypothyroidism; cholesterol ester storage disease;
XX
XX immune deficiency; immune disorder; infectious disease;
XX
XX autoimmune disorder; Rheumatoid arthritis; autoimmune thyroiditis;
XX
XX myasthenia gravis.
XX
XX Homo sapiens.
XX
XX WO200192523-A2.
XX
XX 06-DEC-2001.
XX
XX

PF 29-MAY-2001: 2001WO-US10836.

PR 30-MAY-2000: 2000US-206132P.

PR 29-AUG-2000: 2000US-228716P.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach MD;

DR WPI: 2002-106308/14.

DR N-PSDB; ABN25576.

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

Disclosure; SEQ ID 19630; 1037pp; English.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, osteoarthritis, benign tumors, keloid, degenerative disorders, haemorrhage, transplacental, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester diseases, autoimmune disorders such as multiple sclerosis, infectious arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 60 AA;

Query Match

Best Local Similarity 100.0%; Score 23; DB 23; Length 60;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4

DB 54 NYDA 57

RESULT 39

AAB90301 AAB90301 standard; Protein; 61 AA.

AC AAB90301;

DT 01-JUN-2001 (first entry)

DE Human SAA carboxy truncation, SEQ ID NO: 59.

XX

Human: serum amyloid A; SAA: human formyl peptide receptor variant; FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic; antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;

immune system disorder; amyloidosis; inflammation; infection;

organ rejection; arthritis; atherosclerosis.

OS Homo sapiens.

XX

FN WO200121188-A1.

PD 29-MAR-2001.

PF 22-SEP-1999; 99WO-US21770.

PR 22-SEP-1999; 99WO-US21770.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

DR WPI: 2001-211457/21.

New serum amyloid A and formyl peptide receptor variant complex and its modulators, useful for treating immune system disorders, amyloidosis, inflammation, infection, organ rejection, arthritis, atherosclerosis and neoplasia.

Disclosure; Page 16; 141pp; English.

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Sequence 61 AA;

Query Match

Best Local Similarity 100.0%; Score 23; DB 22; Length 61;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4

DB 42 NYDA 45

RESULT 40

AAB90302 AAB90302 standard; Protein; 62 AA.

AC AAB90302;

DT 01-JUN-2001 (first entry)

DE Human SAA carboxy truncation, SEQ ID NO: 60.

XX

Human: serum amyloid A; SAA: human formyl peptide receptor variant; FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;

antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;

immune system disorder; amyloidosis; inflammation; infection;

organ rejection; arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200121188-A1.

PD 29-MAR-2001.

PF 22-SEP-1999; 99WO-US21770.

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PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

DR WPI: 2001-211457/21.

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 PT and neoplasia -
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 CC invention relates to the discovery that SAA is a ligand for FPR1 (human
 CC formyl peptide receptor variant). A complex has been isolated that
 CC comprises a peptide agent with a sequence corresponding to SAA, or its
 CC conservative variant or functional fragment, bound to FPR1. Modulators
 CC of the SAA/FPR1 complex are useful for treating immune system
 CC disorders, amyloidosis, inflammation, infection, organ rejection,
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
 CC for their ability to modulate assembly of the SAA/FPR1 complex.
 CC
 SQ Sequence 62 AA;
 Query Match 100.0%; Score 23; DB 22; Length 62;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYDA 4
 ||||
 DB 42 NYDA 45
 RESULT 41
 AAB90303
 ID AAB90303 standard; Protein; 63 AA.
 XX AAB90303;
 AC
 XX 01-JUN-2001 (first entry)
 DT
 XX Human SAA carboxy truncation, SEQ ID NO: 61.
 DE
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;
 KM FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
 KM antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
 KM immune system disorder; amyloidosis; inflammation; infection;
 KM organ rejection; arthritis; atherosclerosis.
 KM
 XX Homo sapiens.
 OS
 XX WO200121188-A1.
 PN
 XX 29-MAR-2001.
 PD
 XX 22-SEP-1999; 99WO-US21770.
 PF
 XX 22-SEP-1999; 99WO-US21770.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.
 PI
 XX WPI; 2001-211457/21.
 DR
 XX New serum amyloid A and formyl peptide receptor variant complex and its
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 PT inflammation, infection, organ rejection, arthritis, atherosclerosis
 PT and neoplasia -
 PS Disclosure; Page 16; 141pp; English.
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 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
 CC for their ability to modulate assembly of the SAA/FPR1 complex.
 CC

CC of the SAA/FPR1 complex are useful for treating immune system
 CC disorders, amyloidosis, inflammation, infection, organ rejection,
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
 CC for their ability to modulate assembly of the SAA/FPR1 complex.
 CC
 SQ Sequence 63 AA;
 Query Match 100.0%; Score 23; DB 22; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYDA 4
 ||||
 DB 42 NYDA 45
 RESULT 42
 AAB90304
 ID AAB90304 standard; Protein; 64 AA.
 XX AAB90304;
 AC
 XX 01-JUN-2001 (first entry)
 DT
 XX Human SAA carboxy truncation, SEQ ID NO: 62.
 DE
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;
 KM FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
 KM antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
 KM immune system disorder; amyloidosis; inflammation; infection;
 KM organ rejection; arthritis; atherosclerosis.
 KM
 XX Homo sapiens.
 OS
 XX WO200121188-A1.
 PN
 XX 29-MAR-2001.
 PD
 XX 22-SEP-1999; 99WO-US21770.
 PF
 XX 22-SEP-1999; 99WO-US21770.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
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 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.
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 XX WPI; 2001-211457/21.
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 XX New serum amyloid A and formyl peptide receptor variant complex and its
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 PT and neoplasia -
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 CC The present sequence is a fragment of human serum amyloid A (SAA). The
 CC invention relates to the discovery that SAA is a ligand for FPR1 (human
 CC formyl peptide receptor variant). A complex has been isolated that
 CC comprises a peptide agent with a sequence corresponding to SAA, or its
 CC conservative variant or functional fragment, bound to FPR1. Modulators
 CC of the SAA/FPR1 complex are useful for treating immune system
 CC disorders, amyloidosis, inflammation, infection, organ rejection,
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
 CC for their ability to modulate assembly of the SAA/FPR1 complex.
 CC
 SQ Sequence 64 AA;
 Query Match 100.0%; Score 23; DB 22; Length 64;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYDA 4
 ||||

DB 42 NYDA 45

RESULT 43
ID AAB90383 standard; Protein: 64 AA.

XX AAB90383;
AC AAB90383;
XX 01-JUN-2001 (first entry)
XX

DE Human SAA amino truncation, SEQ ID NO: 141.
XX

KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.

XX Homo sapiens.
OS
XX WO200121188-A1.
XX

PN 29-MAR-2001.
XX

PD 22-SEP-1999; 99WO-US21770.
XX

PF 22-SEP-1999; 99WO-US21770.
XX

PR 22-SEP-1999; 99WO-US21770.
XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

PA Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
XX WPI; 2001-211457/21.
XX

PT New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX

XX Disclosure: Page 20; 141pp; English.
XX

PS The present sequence is a fragment of human serum amyloid A (SAA). The
XX invention relates to the discovery that SAA is a ligand for FPR1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPR1. Modulators
CC of the SAA/FPR1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPR1 complex.
XX

SQ Sequence 64 AA;
XX

Query Match 100.0%; Score 23; DB 22; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
DB 1 NYDA 4

RESULT 44
ID AAB90483 standard; Protein: 64 AA.
XX AAB90483;
AC AAB90483;
XX 01-JUN-2001 (first entry)
XX

DE Human SAA internal truncation, SEQ ID NO: 241.
XX

KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;
KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;
KW antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;
KW immune system disorder; amyloidosis; inflammation; infection;
KW organ rejection; arthritis; atherosclerosis.

XX Homo sapiens.
OS
XX WO200121188-A1.
XX

PN 29-MAR-2001.
XX

PD 22-SEP-1999; 99WO-US21770.
XX

PF 22-SEP-1999; 99WO-US21770.
XX

PR 22-SEP-1999; 99WO-US21770.
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX
XX WPI; 2001-211457/21.
XX

PN New serum amyloid A and formyl peptide receptor variant complex and its
PT modulators, useful for treating immune system disorders, amyloidosis,
PT inflammation, infection, organ rejection, arthritis, atherosclerosis
PT and neoplasia -
XX

XX Disclosure: Page 28; 141pp; English.
XX

PS The present sequence is a fragment of human serum amyloid A (SAA). The
XX invention relates to the discovery that SAA is a ligand for FPR1 (human
CC formyl peptide receptor variant). A complex has been isolated that
CC comprises a peptide agent with a sequence corresponding to SAA, or its
CC conservative variant or functional fragment, bound to FPR1. Modulators
CC of the SAA/FPR1 complex are useful for treating immune system
CC disorders, amyloidosis, inflammation, infection, organ rejection,
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested
CC for their ability to modulate assembly of the SAA/FPR1 complex.
XX

SQ Sequence 64 AA;
XX

Query Match 100.0%; Score 23; DB 22; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
DB 1 NYDA 4

RESULT 45
ID AAM62372 standard; peptide: 65 AA.
XX AAM62372;
AC AAM62372;
XX 01-OCT-1998 (first entry)
XX

DE Antithrombotic peptide SEQ ID NO:19 from WO9825970.
XX

KW Antithrombotic peptide; fibronectin type II repeat; platelet;
KW divalent cation-independent adhesion; vascular injury.
XX

XX Homo sapiens.
OS
XX Synthetic.
XX

PN WO9825970-A1.
XX

PD 18-JUN-1998.
XX

PF 10-DEC-1997; 97WO-US22724.
XX

PR 10-DEC-1996; 96US-0032542.
XX

XX (UNITW) UNIV WASHINGTON.
 PA
 XX
 PI Santoro SA, Staats WD;
 XX
 DR WPI; 1998-348460/30.
 XX
 PT New anti-thrombotic peptide(s) - used to aid in initiation of
 PT recovery from vascular injury
 XX
 PS Example; Fig 3; 55pp; English.
 XX
 CC The present sequence represents a peptide from the example of the
 CC present invention, which describes antithrombotic peptides derived
 CC from human fibronectin type II repeats. The peptides can mediate
 CC divalent cation-independent adhesion of platelets to fibronectin.
 CC They can therefore be used to aid in the initiation of recovery from
 CC vascular injury.
 XX

SQ Sequence 65 AA;

Query Match 100.0%; Score 23; DB 19; Length 65;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 47 NYDA 50

Search completed: February 6, 2003, 11:19:41
 Job time : 28.8333 secs

Thu Feb 6 12:30:18 2003

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 ; Search time 9.33333 Seconds
(Without alignments)
12.610 Million cell updates/sec

Title: pat943-5
Perfect score: 23
Sequence: 1 nyda 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 108

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA:*
1: /cgn2_6/pdata1/1/aa/5A.COMB.pep.*
2: /cgn2_6/pdata1/1/aa/5B.COMB.pep.*
3: /cgn2_6/pdata1/1/aa/6A.COMB.pep.*
4: /cgn2_6/pdata1/1/aa/6B.COMB.pep.*
5: /cgn2_6/pdata1/1/aa/CTUS.COMB.pep.*
6: /cgn2_6/pdata1/1/aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	23	100.0	7	US-09-296-284-13	Sequence 13, Appl
2	23	100.0	16	US-08-752-844-6	Patent No. 5180819
3	23	100.0	19	US-08-752-844-6	Sequence 6, Appl
4	23	100.0	19	US-08-591-186-6	Sequence 19, Appl
5	23	100.0	65	US-08-982-597A-19	Sequence 19, Appl
6	23	100.0	65	US-09-136-218-19	Sequence 2, Appl
7	23	100.0	100	US-08-384-367-2	Sequence 1, Appl
8	23	100.0	104	US-09-029-345-1	Sequence 82, Appl
9	23	100.0	122	US-09-154-750A-82	Sequence 4639, Ap
10	23	100.0	149	US-09-134-001C-4639	Sequence 4, Appl
11	23	100.0	152	US-08-752-844-4	Sequence 4, Appl
12	23	100.0	152	US-08-591-186-4	Sequence 4, Appl
13	23	100.0	152	US-09-192-838B-4	Sequence 2, Appl
14	23	100.0	154	US-09-491-916-22	Sequence 4, Appl
15	23	100.0	175	US-09-129-030-22	Sequence 4747, Ap
16	23	100.0	175	US-09-134-001C-4747	Sequence 4623, Ap
17	23	100.0	178	US-09-134-001C-4623	Sequence 339, Ap
18	23	100.0	191	US-08-858-207A-339	Patent No. 5180819
19	23	100.0	214	US-08-858-207A-339	Patent No. 5180819
20	23	100.0	215	US-08-394-600B-20	Sequence 30, Appl
21	23	100.0	229	US-08-944-483-30	Sequence 20, Appl
22	23	100.0	229	US-08-944-483-30	Sequence 20, Appl
23	23	100.0	230	US-09-02513-20	Sequence 18, Appl
24	23	100.0	230	US-09-230-196-18	Sequence 23, Appl
25	23	100.0	230	US-09-230-196-23	Sequence 80, Appl
26	23	100.0	250	US-08-378-761A-80	Sequence 80, Appl
27	23	100.0	250	US-08-485-286-80	Sequence 80, Appl

pat943-5.ra1

28	23	100.0	256	2	US-08-230-428B-4	Sequence 4, Appl
29	23	100.0	263	2	US-08-752-844-66	Sequence 66, Appl
30	23	100.0	280	2	US-09-296-284-27	Sequence 27, Appl
31	23	100.0	292	2	US-08-555-568B-19	Sequence 19, Appl
32	23	100.0	292	4	US-09-519-223-13	Sequence 13, Appl
33	23	100.0	306	1	US-08-368-852-13	Sequence 13, Appl
34	23	100.0	306	2	US-08-525-940-13	Sequence 13, Appl
35	23	100.0	306	2	US-08-976-838-13	Sequence 6, Appl
36	23	100.0	306	2	US-09-296-284-6	Sequence 3, Appl
37	23	100.0	355	4	US-09-000-064-2	Sequence 2, Appl
38	23	100.0	383	4	US-09-627-650B-20	Sequence 20, Appl
39	23	100.0	404	4	US-09-134-001C-4848	Sequence 4848, Ap
40	23	100.0	429	2	US-09-074-512-1	Sequence 1, Appl
41	23	100.0	447	1	US-08-844-010-2	Sequence 2, Appl
42	23	100.0	447	3	US-09-012-873-2	Sequence 3354, Ap
43	23	100.0	456	4	US-09-134-001C-3354	Sequence 4, Appl
44	23	100.0	474	1	US-08-459-100A-4	Sequence 4, Appl
45	23	100.0	474	1	US-08-459-100A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-296-284-13 Application US/09296284A
Sequence 13, Appl
Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eun-Sung
APPLICANT: Choi, Sang-Ki
APPLICANT: Rhee, Eun-Hae
TITLE OF INVENTION: Glucosyltransferase Subunits Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 7
TYPE: PRT
ORGANISM: Glucosyltransferase suboxydians
US-09-296-284-13

Query Match 100.0%; Score 23; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 1 NYDA 4

RESULT 2
5180819-6
Patent No. 5180819
APPLICANT: CAYRE, YVON
TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
MOLECULE ENCODING SAME, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICANT: CAYRE, YVON
FILING DATE: 22-DEC-1989
SEQ ID NO: 6
LENGTH: 16
5180819-6

Query Match 100.0%; Score 23; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
1111

Db 5 NYDA 8

RESULT 3

US-08-752-844-6

Sequence 6, Application US/08752844

Patent No. 5935821

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Foon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/752,844

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Schiff, J. Michael

REGISTRATION NUMBER: 40,253

REFERENCE/DOCKET NUMBER: 30414-20002.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-752-844-6

Query Match

Best Local Similarity 100.0%; Score 23; DB 2; Length 19;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4

Db 2 NYDA 5

RESULT 4

US-08-591-196-6

Sequence 6, Application US/08591196

Patent No. 597316

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Foon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

Query Match

Best Local Similarity 100.0%; Score 23; DB 2; Length 19;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4

Db 2 NYDA 5

RESULT 5

US-08-982-597A-19

Sequence 19, Application US/08982597A

Patent No. 5932693

GENERAL INFORMATION:

APPLICANT: Santoro, Samuel A.

APPLICANT: Statz, William D.

TITLE OF INVENTION: Antithrombotic Peptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scott J. Meyer

STREET: 800 No. 5932693th Lindbergh Blvd.

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/982,597A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032,542

FILING DATE: 10-DEC-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Meyer, Scott J.

REGISTRATION NUMBER: 25,275

REFERENCE/DOCKET NUMBER: WU-3002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-694-3117

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 65 amino acids

TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-982-597A-19

Query Match 100.0%; Score 23; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 47 NYDA 50

RESULT 6

US-09-136-218-19
Sequence 19, Application US/09136218
Patent No. 6083914
GENERAL INFORMATION:
APPLICANT: Santoro, Samuel A.
APPLICANT: Straetz, William D.
TITLE OF INVENTION: Antithrombotic Peptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer
STREET: 800 No. 6083914th Lindbergh Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,218
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/982,597
FILING DATE:
APPLICATION NUMBER: 60/032,542
FILING DATE: 10-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: WU-3002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-694-3117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-136-218-19

Query Match 100.0%; Score 23; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 47 NYDA 50

RESULT 7
US-08-384-367-2
Sequence 2, Application US/08384367
Patent No. 5629469
GENERAL INFORMATION:
APPLICANT: Deluca-Flaherty, Camille
APPLICANT: Chan, Victor J.

APPLICANT: Scarafia C., Lilliana E.
APPLICANT: Brunke, Karen J.
TITLE OF INVENTION: NOVEL THIOL PROTEASE INHIBITOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc.
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,367
FILING DATE: 10-FEB-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,571
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 135-1088/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/857-1125
TELEFAX: 415/354-3588
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-384-367-2

Query Match 100.0%; Score 23; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 35 NYDA 38

RESULT 8

US-09-029-345-1
Sequence 1, Application US/09029345B
Patent No. 6375949
GENERAL INFORMATION:
APPLICANT: Hirano, et al.
TITLE OF INVENTION: Monoclonal Antibody Recognizing Serum Amyloid A
FILE REFERENCE: 112842-100
CURRENT APPLICATION NUMBER: US/09/029,345B
CURRENT FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
US-09-029-345-1

Query Match 100.0%; Score 23; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 41 NYDA 44

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RESULT 9
US-09-154-750A-82
; Sequence 82, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-750A-82

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Query Match      100.0%; Score 23; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 NYDA 4
    ||||
Db 59 NYDA 62

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```

RESULT 10
US-09-134-001C-4639
; Sequence 4639, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4639
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4639

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Query Match      100.0%; Score 23; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 NYDA 4
    ||||
Db 68 NYDA 71

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RESULT 11
US-08-752-844-4
; Sequence 4, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.

```

```

; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-4

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Query Match      100.0%; Score 23; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 NYDA 4
    ||||
Db 119 NYDA 122

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RESULT 12
US-08-591-196-4
; Sequence 4, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael

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?      REGISTRATION NUMBER: 40,253
?      REFERENCE/DOCKET NUMBER: 30414-20002.20
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (415) 813-5600
?      TELEFAX: (415) 494-0792
?      TELEEX: 706141
?      INFORMATION FOR SEQ ID NO: 4:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 152 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      US-08-591-196-4

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Query Match	100.0%;	Score 23;	DB 2;	Length 152;
Best Local Similarity	100.0%;	Pred. No. 2e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	NYDA	4
Db	119	NYDA	122

RESULT 13
US-09-192-838B-4
; Sequence 4, Application US/09192838B
Data4 was 03504

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? APPLICANT: CHATTERJEE, Malaya
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
? FILE REFERENCE: 304142000500
? CURRENT APPLICATION NUMBER: US/09/192,838B
? CURRENT FILING DATE: 1998-11-16
? PRIOR APPLICATION NUMBER: 60/065,774
? PRIOR FILING DATE: 1997-11-17
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 4
? LENGTH: 152
? TYPE: PR1
? ORGANISM: Mus Musculus
? SS-09-192-838B-4

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Query Match	100.0%;	Score 23;	DB 4;	Length 152;
Best Local Similarity	100.0%;	Pred. No. 2e+02;		
Matches	4;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;);

QY	1	NYDA	4
Db	119	NYDA	122

RESULT 14
US-09-491-916-2
; Sequence 2, Application US/09491916

GENERAL INFORMATION:
APPLICANT: Palmer, Leslie M.
TITLE OF INVENTION: NO. 6326462el r1bh
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Street
CITY: Philadelphia

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?      COUNTRY: US
?      ZIP: 19103
?
?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: diskette
?      COMPUTER: IBM Compatible
?      OPERATING SYSTEM: DOS
?      SOFTWARE: FastSeq for Windows Version 2.0

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,916
FILING DATE: 27-Jan-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA: 00,000,000

APPLICATION NUMBER: 08/977,553
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dickerson Todd C

REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10123
TELECOMMUNICATION INFORMATION:
TEL EDUONE: 315-004-3353

TELEFAX: 215-994-2222
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION:	SEQ ID NO:
US-09-491-916-2	2:

Query Match	100.0%;	Score 23;	DB 4;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 2.1e+02;		
Matches	4;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;

QY	1	NYDA	4
Db	70	NYDA	73

RESULT 15
US-09-129-030-22
Sequence 22, Application US/09129030A

```
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
; TITLE OF INVENTION: GENOMIC PPO CLONES
; FILING DATE: 07/09/88
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 175
; TYPE: PRT
; ORGANISM: PEAR
US-09-129-030-22

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Query Match	100.0%;	Score 23;	DB 4;	Length 175;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
Matches	4;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;

QY	1	NYDA	4
Db	10	NYDA	13

RESULT 16
US-09-134-001C-4747

Sequence 4747, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucet-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

;; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: GTC-007
;; CURRENT APPLICATION NUMBER: US/09/134,001C
;; CURRENT FILING DATE: 1998-08-13
;; PRIOR APPLICATION NUMBER: US 60/064,964
;; PRIOR FILING DATE: 1997-11-08
;; PRIOR APPLICATION NUMBER: US 60/055,779
;; PRIOR FILING DATE: 1997-08-14
;; NUMBER OF SEQ ID NOS: 5674
;; SEQ ID NO 4747
;; LENGTH: 175
;; TYPE: PRT
;; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4747

Query Match 100.0%; Score 23; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 67 NYDA 70

RESULT 17
US-09-134-001C-4623
; Sequence 4623, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4623
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4623

Query Match 100.0%; Score 23; DB 4; Length 178;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 147 NYDA 150

RESULT 18
US-08-858-207A-339
; Sequence 339, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

;; ZIP: 19406-0939
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/858,207A
;; FILING DATE: 09-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/017670
;; FILING DATE: 14-MAY-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gimm, Edward R
;; REGISTRATION NUMBER: 38,891
;; REFERENCE/DOCKET NUMBER: P50475
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-4478
;; TELEFAX: 610-270-5090
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 339:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 191 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 6348328e
US-08-858-207A-339

Query Match 100.0%; Score 23; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 117 NYDA 120

RESULT 19
5180819-3
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO:3:
; LENGTH: 214
5180819-3

Query Match 100.0%; Score 23; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 68 NYDA 71

RESULT 20
5180819-2
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO:2:

LENGTH: 215
5180819-2

Query Match 100.0%; Score 23; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
DB 68 NYDA 71

RESULT 21

US-08-394-600B-20
; Sequence 20, Application US/08394600B
; Patent No. 5843693
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; APPLICANT: Jewell, David A.
; APPLICANT: Koths, Kirston E.
; APPLICANT: Kriegluer, Michael
; APPLICANT: Perez, Carl
; TITLE OF INVENTION: Compositions for the inhibition of
; TITLE OF INVENTION: Protein Hormone Formation and Uses Thereof
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street; 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,600B
; FILING DATE: 02/27/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Donald J. Pochoplen
; REGISTRATION NUMBER: 32,167
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-394-600B-20

Query Match 100.0%; Score 23; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
DB 82 NYDA 85

RESULT 22
US-08-944-483-30
; Sequence 30, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6232456e
US-08-944-483-30

Query Match 100.0%; Score 23; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
DB 82 NYDA 85

RESULT 23

PCT-US95-02513-20
; Sequence 20, Application PC/TUS9502513
; GENERAL INFORMATION:
; APPLICANT: Halenbeck, Robert F.
; APPLICANT: Jewell, David A.
; APPLICANT: Koths, Kirston E.
; APPLICANT: Kriegluer, Michael
; APPLICANT: Perez, Carl
; TITLE OF INVENTION: Compositions for the inhibition of
; TITLE OF INVENTION: Protein Hormone Formation and Uses Thereof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02513
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27527/32404
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02513-20

Query Match 100.0%; Score 23; DB 5; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 82 NYDA 85

RESULT 24
US-09-230-196-18
Sequence 18, Application US/09230196
Patent No. 6307035
GENERAL INFORMATION:
APPLICANT: Rauscher III, Frank J.
APPLICANT: Jensen, David E.
TITLE OF INVENTION: BRCA1 Associated Protein (BAP-1) and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/230,196
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,997
FILING DATE: 02-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,109
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST68BUSA
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-230-196-18

Query Match 100.0%; Score 23; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 140 NYDA 143

RESULT 25
US-09-230-196-23
Sequence 23, Application US/09230196
Patent No. 6307035
GENERAL INFORMATION:
APPLICANT: Rauscher III, Frank J.
APPLICANT: Jensen, David E.
TITLE OF INVENTION: BRCA1 Associated Protein (BAP-1) and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/230,196
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,997
FILING DATE: 02-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,109
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST68BUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-230-196-23

Query Match 100.0%; Score 23; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4

Db 140 NYDA 143

RESULT 26

US-08-378-761A-80
Sequence 80, Application US/08378761A
Patent No. 5635384

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS

STATE: IN
COUNTRY: US

ZIP: 46268

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T

REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-378-761A-80

OY 1 NYDA 4

Db 55 NYDA 58

RESULT 27

US-08-485-286-80
Sequence 80, Application US/08485286
Patent No. 5646026

Patent No. 5646026 5646119
GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS

STATE: IN
COUNTRY: US

ZIP: 46268

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,286
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761

FILING DATE: 26-JAN-1995

ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T

REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-286-80

OY 1 NYDA 4

Db 55 NYDA 58

RESULT 28

US-08-230-428B-4

Sequence 4, Application US/08230428B
Patent No. 5998378

GENERAL INFORMATION:

APPLICANT: Kriegluer, Michael
APPLICANT: Perez, Carl

APPLICANT: Halenbeck, Robert F.
APPLICANT: Jewell, David A.

APPLICANT: Kohls, Kirston E.
TITLE OF INVENTION: Compositions For The Inhibition Of TNF

TITLE OF INVENTION: Hormone Formation And Uses Thereof (As Amended)

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
STREET: 4560 Horton Street, P.O. Box 8097
CITY: Emeryville

STATE: California

COUNTRY: United States of America
ZIP: 94662-8097

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/230,428B
FILING DATE: 19-APR-1994

CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,546
FILING DATE: 25-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/395,253

FILING DATE: 16-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0820.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-230-428B-4

Query Match 100.0%; Score 23; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 109 NYDA 112

RESULT 29
US-08-752-844-66
Sequence 66, Application US/08752844
Patent No. 5935821
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Poon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-752-844-66

Query Match 100.0%; Score 23; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYDA 4

DB 119 NYDA 122

RESULT 30
US-09-296-284-27
Sequence 27, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eun-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Glucanobacter suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of use thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 27
LENGTH: 280
TYPE: PRT
ORGANISM: Glucanobacter suboxydans
US-09-296-284-27

Query Match 100.0%; Score 23; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 107 NYDA 110

RESULT 31
US-08-555-568B-19
Sequence 19, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-3851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-19

Query Match 100.0%; Score 23; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
1111
Db 151 NYDA 154

RESULT 32

US-09-519-223-19
Sequence 19, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-519-223-19

Query Match 100.0%; Score 23; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
1111
Db 151 NYDA 154

RESULT 33

US-08-368-852-13
Sequence 13, Application US/08368852
Patent No. 5691183
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,852
FILING DATE: 05-JAN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2848-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-368-852-13

Query Match 100.0%; Score 23; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
1111
Db 49 NYDA 52

RESULT 34

US-08-525-940-13
Sequence 13, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-13

Query Match 100.0%; Score 23; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 49 NYDA 52

RESULT 35
US-08-976-838-13
Sequence 13, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-13

Query Match 100.0%; Score 23; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 49 NYDA 52

RESULT 36
US-09-296-284-6
Sequence 6, Application US/09296284A

Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eun-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Glucobacter Suboxydans Sorbitol Dehydrogenase, Genes
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 306
TYPE: PRT
ORGANISM: Glucobacter suboxydans
US-09-296-284-6

Query Match 100.0%; Score 23; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 133 NYDA 136

RESULT 37
US-09-000-040-3
Sequence 3, Application US/09000040B
Patent No. 6180388
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: FAUCHER, Didier
APPLICANT: FAVRE-BULLE, Olivier
APPLICANT: JOURDAT, Catherine
APPLICANT: PETRE, Dominique
APPLICANT: PIERARD, Jerome
APPLICANT: THIBAUT, Denis
APPLICANT: GUTTON, Carole
TITLE OF INVENTION: ENZYMES AND MICRO-ORGANISMS WITH AMIDASE ACTIVITY WHICH
FILE REFERENCE: 003025-035
CURRENT APPLICATION NUMBER: US/09/000,040B
CURRENT FILING DATE: 1998-04-03
EARLIER APPLICATION NUMBER: FR 95/08917
EARLIER FILING DATE: 1995-07-18
EARLIER APPLICATION NUMBER: PCT/FR96/01118
EARLIER FILING DATE: 1996-07-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 355
TYPE: PRT
ORGANISM: Comamonas acidovorans
US-09-000-040-3

Query Match 100.0%; Score 23; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 235 NYDA 238

RESULT 38
US-09-000-064-2
Sequence 2, Application US/09000064
Patent No. 6214592
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: FAVRE-BULLE, Olivier

APPLICANT: Jourdat, Catherine
APPLICANT: le Coq, Anne-Marie
APPLICANT: Petre, Dominique
TITLE OF INVENTION: ENZYMES AND MICROORGANISMS HAVING AMIDASE ACTIVITY FOR
FILE OF INVENTION: HYDROLYSING POLYAMIDES
FILE REFERENCE: 003025-036
CURRENT APPLICATION NUMBER: US/09/000,064
CURRENT FILING DATE: 1998-04-03
EARLIER APPLICATION NUMBER: PCT/FR96/01119
EARLIER FILING DATE: 1996-07-17
EARLIER APPLICATION NUMBER: FR 9508916
EARLIER FILING DATE: 1995-07-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 355
TYPE: PRT
ORGANISM: Escherichia coli
US-09-000-064-2

Query Match 100.0%; Score 23; DB 4; Length 355;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 235 NYDA 238

RESULT 39
US-09-627-650B-20
Sequence 20, Application US/09627650B
Patent No. 6405872
GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.000903
CURRENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107,727
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 383
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/note =
OTHER INFORMATION: synthetic construct
US-09-627-650B-20

Query Match 100.0%; Score 23; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 267 NYDA 270

RESULT 40
US-09-134-001C-4848
Sequence 4848, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4848
LENGTH: 404
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4848

Query Match 100.0%; Score 23; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 176 NYDA 179

RESULT 41
US-09-074-512-1
Sequence 1, Application US/09074512
Patent No. 5952479
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN ARSENITE-RESISTANCE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,512
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0518 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVARUTUT01
CLONE: 2257452
US-09-074-512-1

Query Match 100.0%; Score 23; DB 2; Length 429;

Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 388 NYDA 391

RESULT 42

US-08-844-010-2

; Sequence 2, Application US/08844010

; Patent No. 5753480

; GENERAL INFORMATION:

; APPLICANT: Lawlor, Elizabeth

; TITLE OF INVENTION: No. 5753480e1 Compounds

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/844,010

; FILING DATE: 18-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 9607991.8

; FILING DATE: 18-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Gimmil, Edward R

; REGISTRATION NUMBER: 38,891

; REFERENCE/DOCKET NUMBER: P31458-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-4478

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 447 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-844-010-2

Query Match 100.0%; Score 23; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 373 NYDA 376

RESULT 43

US-09-012-873-2

; Sequence 2, Application US/09012873

; Patent No. 6074858

; GENERAL INFORMATION:

; APPLICANT: Lawlor, Elizabeth

; TITLE OF INVENTION: No. 6074858e1 Compounds

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

STATE: PA
COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/012,873

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/844,010

FILING DATE: 18-APR-1997

APPLICATION NUMBER: 9607991.8

FILING DATE: 18-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Gimmil, Edward R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P31458-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 447 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-012-873-2

Query Match 100.0%; Score 23; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 373 NYDA 376

RESULT 44

US-09-134-001C-3354

; Sequence 3354, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3354

; LENGTH: 456

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3354

Query Match 100.0%; Score 23; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 81 NYDA 84

RESULT 45
US-08-459-100A-4
; Sequence 4, Application US/08459100A
; Patent No. 5654172
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunit
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARBLLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,100A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09589
; FILING DATE: 26 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-325
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-459-100A-4

Query Match 100.0%; Score 23; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
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Db 268 NYDA 271

Search completed: February 6, 2003, 11:24:09
Job time : 11.3333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:22:09 : Search time 5.83333 Seconds
(without alignments)
15.202 Million cell updates/sec

Title: PAT943-5
Perfect score: 23
Sequence: 1 nyda 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 129505 seqs, 22169297 residues
Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*

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- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	100.0	28	10	US-09-864-761-43895
2	23	100.0	36	10	US-09-864-761-35859
3	23	100.0	72	10	US-09-864-761-43317
4	23	100.0	122	10	US-09-853-386-102
5	23	100.0	146	9	US-10-047-260-14
6	23	100.0	152	10	US-09-990-205-4
7	23	100.0	167	10	US-09-925-300-981
8	23	100.0	230	12	US-10-029-630-4
9	23	100.0	236	9	US-09-738-626-4034
10	23	100.0	292	10	US-09-927-180-19
11	23	100.0	343	10	US-09-934-706-1
12	23	100.0	370	10	US-09-804-551B-6
13	23	100.0	400	10	US-09-934-706-5
14	23	100.0	404	9	US-09-738-626-5170
15	23	100.0	423	10	US-09-815-242-5817
16	23	100.0	463	9	US-09-738-626-4947
17	23	100.0	500	9	US-10-157-855-17
18	23	100.0	501	10	US-09-934-706-4
19	23	100.0	539	9	US-09-738-626-6722

20	23	100.0	546	10	US-09-815-242-5510	Sequence 5510, Ap
21	23	100.0	549	10	US-09-815-242-12592	Sequence 12592, A
22	23	100.0	551	10	US-09-529-063-79	Sequence 79, Appl
23	23	100.0	576	10	US-09-841-132-523	Sequence 523, App
24	23	100.0	576	12	US-10-007-693-73	Sequence 73, Appl
25	23	100.0	578	10	US-09-815-242-13023	Sequence 13023, A
26	23	100.0	599	9	US-10-108-605-99	Sequence 99, Appl
27	23	100.0	599	9	US-10-108-605-163	Sequence 163, App
28	23	100.0	606	10	US-09-750-703-4	Sequence 4, Appl
29	23	100.0	647	9	US-09-738-626-6180	Sequence 6180, Ap
30	23	100.0	687	9	US-09-969-384-16	Sequence 16, Appl
31	23	100.0	687	9	US-09-969-384-27	Sequence 27, Appl
32	23	100.0	687	10	US-09-927-180-21	Sequence 21, Appl
33	23	100.0	688	10	US-09-927-180-23	Sequence 23, Appl
34	23	100.0	708	10	US-09-925-301-1012	Sequence 1012, Ap
35	23	100.0	711	9	US-09-738-626-3507	Sequence 3507, Ap
36	23	100.0	721	9	US-09-764-868-731	Sequence 731, App
37	23	100.0	739	9	US-09-738-626-6988	Sequence 6988, Ap
38	23	100.0	752	10	US-09-927-180-2	Sequence 2, Appl
39	23	100.0	805	10	US-09-841-132-386	Sequence 386, App
40	23	100.0	897	10	US-09-815-242-12769	Sequence 12769, A
41	23	100.0	904	10	US-09-801-368-272	Sequence 272, App
42	23	100.0	1113	10	US-09-815-242-5836	Sequence 5836, Ap
43	23	100.0	1136	10	US-09-815-242-12447	Sequence 12447, A
44	23	100.0	1136	10	US-09-815-242-12814	Sequence 12814, A
45	23	100.0	1179	10	US-09-815-242-5522	Sequence 5522, Ap

ALIGNMENTS

RESULT 1
US-09-864-761-43895
; Sequence 43895, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43895
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005083.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.43
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
; US-09-864-761-43895
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Query Match          100.0%; Score 23; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 NYDA 4
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Db       7 NYDA 10
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RESULT 2
US-09-864-761-35859
; Sequence 35859, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35859
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EST_HUMAN HIT: AF403965.1, EVALU0 2.00e-13
; US-09-864-761-35859
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 NYDA 4
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Db       30 NYDA 33
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RESULT 3
US-09-864-761-43317
; Sequence 43317, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43317
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004983.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.86
OTHER INFORMATION: EST_HUMAN HIT: AA323348.1, EVALUATE 2.00e-21
US-09-864-761-43317

Query Match 100.0%; Score 23; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
1111
DB 60 NYDA 63
RESULT 4
US-09-853-386-102
Sequence 102, Application US/09853386
Patent No. US20020049151A1
GENERAL INFORMATION:
APPLICANT: Murphy, Evelyn
APPLICANT: Bresnahan, Barry
APPLICANT: Conneely, Orla
APPLICANT: Fitzgerald, Oliver
TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REFERENCE: P01972051
CURRENT APPLICATION NUMBER: US/09/853,386
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/203645
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PatentIn version 3.1
SEQ ID NO 102
LENGTH: 122
TYPE: PRT
ORGANISM: HUMAN
US-09-853-386-102

Query Match 100.0%; Score 23; DB 10; Length 122;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
1111
DB 59 NYDA 62

RESULT 5
US-10-047-260-14
Sequence 14, Application US/10047260
Patent No. US20020164706A1
GENERAL INFORMATION:
APPLICANT: Huang, Lisa
APPLICANT: McCluskey, Michael
APPLICANT: Larossa, Robert
TITLE OF INVENTION: HIGH LEVEL PROMOTERS FROM CYANOBACTERIA
FILE REFERENCE: C11715 US NA
CURRENT APPLICATION NUMBER: US/10/047,260
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/264,925
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 146
TYPE: PRT
ORGANISM: Synecchocystis sp. strain PCC6803
US-10-047-260-14

Query Match 100.0%; Score 23; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
1111
DB 120 NYDA 123

RESULT 6
US-09-990-205-4
Sequence 4, Application US/09990205
Patent No. US20020150572A1
GENERAL INFORMATION:
APPLICANT: FOON, Kenneth A.
APPLICANT: CHATTERJEE, Malaya
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000501
CURRENT APPLICATION NUMBER: US/09/990,205
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: U.S. 09/192,838
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: U.S. 60/065,774
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 152
TYPE: PRT
ORGANISM: Mus Musculus
US-09-990-205-4

Query Match 100.0%; Score 23; DB 10; Length 152;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
1111
DB 119 NYDA 122
RESULT 7
US-09-925-300-981
Sequence 981, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101

;; CURRENT APPLICATION NUMBER: US/09/925,300
;; CURRENT FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05988
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 1890
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 981
;; LENGTH: 167
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (70)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (162)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-981

Query Match 100.0%; Score 23; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 80 NYDA 83

RESULT 8
US-10-029-630-4
;; Sequence 4, Application US/10029630
;; Patent No. US20020137099A1
;; GENERAL INFORMATION:
;; APPLICANT: Boehringer Ingelheim Pharma KG
;; TITLE OF INVENTION: Method for identifying substances which positively
;; FILE REFERENCE: 1/1179
;; CURRENT APPLICATION NUMBER: US/10/029,630
;; PRIOR FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: US 60/257,856
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 230
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-029-630-4

Query Match 100.0%; Score 23; DB 12; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 140 NYDA 143

RESULT 9
US-09-738-626-4034
;; Sequence 4034, Application US/09738626
;; Publication No. US20020197605A1
;; GENERAL INFORMATION:
;; APPLICANT: NAKAGAWA, SATOSHI
;; APPLICANT: MIZOGUCHI, HIROSHI
;; APPLICANT: ANDO, SEIKO
;; APPLICANT: HAYASHI, MIKIRO
;; APPLICANT: OCHIAI, KEIKO
;; APPLICANT: YOKOI, HARUHIKO
;; APPLICANT: TATEISHI, NAOKO
;; APPLICANT: SENOH, AKIHIRO

;; APPLICANT: IKEDA, MASATO
;; APPLICANT: OZAKI, AKIO
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-125
;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: Patentln ver. 3.0
;; SEQ ID NO 4034
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4034

Query Match 100.0%; Score 23; DB 9; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 37 NYDA 40

RESULT 10
US-09-927-180-19
;; Sequence 19, Application US/09927180
;; Patent No. US20020106364A1
;; GENERAL INFORMATION:
;; APPLICANT: Jones, Simon
;; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Genetics Institute, Inc.
;; STREET: 87 Cambridgepark Drive
;; CITY: Cambridge
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02140
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk.
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/927,180
;; FILING DATE: 09-Aug-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/519,223
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brown, Scott A.
;; REGISTRATION NUMBER: 32,724
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8224
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 292 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 100.0%; Score 23; DB 10; Length 292;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4
||||
Db 151 NYDA 154

RESULT 11
US-09-934-706-1
; Sequence 1, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Terumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934,706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Modified Human
; OTHER INFORMATION: Fibronectin Collagen-Binding Domain
; NAME/KEY: INIT_MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2)..(341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: CONFLICT
; LOCATION: (69)
; NAME/KEY: CONFLICT
; LOCATION: (125)
US-09-934-706-1

Query Match 100.0%; Score 23; DB 10; Length 343;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4
||||
Db 162 NYDA 165

RESULT 12
US-09-804-551B-6
; Sequence 6, Application US/09804551B
; Patent No. US20020056151A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Receptors for peptides from insects
; FILE REFERENCE: Le A 34 394
; CURRENT APPLICATION NUMBER: US/09/804,551B
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: DE 100 13 618-4
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-804-551B-6

Query Match 100.0%; Score 23; DB 10; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4

Db 106 NYDA 109
||||

RESULT 13
US-09-934-706-5
; Sequence 5, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Terumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934,706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Hybrid
; OTHER INFORMATION: Polypeptide of Human Fibronectin Collagen-Binding
; NAME/KEY: INIT_MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2)..(341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(347)
; OTHER INFORMATION: /note=" enterokinase recognition sequence"
; NAME/KEY: PEPTIDE
; LOCATION: (348)..(400)
; OTHER INFORMATION: /note="human epidermal growth factor"
US-09-934-706-5

Query Match 100.0%; Score 23; DB 10; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4
||||
Db 162 NYDA 165

RESULT 14
US-09-738-626-5170
; Sequence 5170, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059

```
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5170
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5170
```

```
Query Match          100.0%; Score 23; DB 9; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
        |||||
DB      164 NYDA 167
```

```
RESULT 15
US-09-815-242-5817
; Sequence 5817, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Cair, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
```

```
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5817
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(423)
; OTHER INFORMATION: xaa = Any Amino Acid
US-09-815-242-5817
```

```
Query Match          100.0%; Score 23; DB 10; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
        |||||
DB      33 NYDA 36
```

```
RESULT 16
US-09-738-626-4947
; Sequence 4947, Application US/09738626
; Publication No. US20020197605A1
```

```
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4947
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4947
```

```
Query Match          100.0%; Score 23; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
        |||||
DB      379 NYDA 382
```

```
RESULT 17
US-10-157-855-17
; Sequence 17, Application US/10157855
; Patent No. US20020170091A1
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael W.
; APPLICANT: Ruzelsky, Diane M.
; TITLE OF INVENTION: Acyl-CoA:cholesterol Acyltransferase Related Nucleic
; FILE REFERENCE: 16516.158
; CURRENT APPLICATION NUMBER: US/10/157,855
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 09/326,203
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-157-855-17
```

```
Query Match          100.0%; Score 23; DB 9; Length 500;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
        |||||
DB      493 NYDA 496
```

```
RESULT 18
US-09-934-706-4
; Sequence 4, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Terumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-Binding
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934,706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Hybrid
; OTHER INFORMATION: Polypeptide of Human Fibronectin Collagen-Binding
; OTHER INFORMATION: Domain and Human Basic Fibroblast Growth Factor
; NAME/KEY: INIT_MBT
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2)..(341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(347)
; OTHER INFORMATION: /note="enterokinase recognition sequence"
; NAME/KEY: PEPTIDE
; LOCATION: (348)..(501)
; OTHER INFORMATION: /note="human fibroblast growth factor"
US-09-934-706-4

Query Match          100.0%; Score 23; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6722
Query Match          100.0%; Score 23; DB 9; Length 539;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
      ||||
DB      252 NYDA 255

RESULT 20
US-09-815-242-5510
; Sequence 5510, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5510
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5510

Query Match          100.0%; Score 23; DB 10; Length 546;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
      ||||
DB      528 NYDA 531

RESULT 21
US-09-815-242-12592
; Sequence 12592, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
```

```
APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA 011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12592
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12592
```

```
Query Match          100.0%; Score 23; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 528 NYDA 531
```

```
RESULT 22
US-09-529-063-79
; Sequence 79, Application US/09529063
; Patent No. US20020102542A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, DAIKICHI
; APPLICANT: SHIBAYAMA, SHIRO
; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
; TITLE OF INVENTION: THE BOTH
; FILE REFERENCE: Q58769
; CURRENT APPLICATION NUMBER: US/09/529,063
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/JP98/04514
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: JP 9-274674
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-063-79
```

```
Query Match          100.0%; Score 23; DB 10; Length 551;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 31 NYDA 34
```

```
RESULT 23
US-09-841-132-523
```

```
; Sequence 523, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: PROBST, PETER
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 523
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-841-132-523
```

```
Query Match          100.0%; Score 23; DB 10; Length 576;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 171 NYDA 174
```

```
RESULT 24
US-10-007-693-73
; Sequence 73, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007,693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 73
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-007-693-73
```

```
Query Match          100.0%; Score 23; DB 12; Length 576;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 171 NYDA 174
```

```
RESULT 25
US-09-815-242-13023
; Sequence 13023, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
```

```
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13023
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-13023
```

```
Query Match          100.0%; Score 23; DB 10; Length 578;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 NYDA 4
    ||||
Db 180 NYDA 183
```

```
RESULT 26
; US-10-108-605-99
; Sequence 99, Application US/10108605
; Patent No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-10-108-605-99
```

```
Query Match          100.0%; Score 23; DB 9; Length 599;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 NYDA 4
    ||||
Db 71 NYDA 74
```

```
RESULT 27
; US-10-108-605-163
; Sequence 163, Application US/10108605
; Patent No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
```

```
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-10-108-605-163
```

```
Query Match          100.0%; Score 23; DB 9; Length 599;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 NYDA 4
    ||||
Db 71 NYDA 74
```

```
RESULT 28
; US-09-750-703-4
; Sequence 4, Application US/09750703
; Patent No. US20020065404A1
; GENERAL INFORMATION:
; APPLICANT: Betenbaugh, Michael
; APPLICANT: Palter, Karen
; TITLE OF INVENTION: CYTIDINE MONOPHOSPHATE-SIALIC ACID TRANSPORTER, AND HEXOSAMINE
; FILE REFERENCE: 03940041A (1100394-0060)
; CURRENT APPLICATION NUMBER: US/09/750,703
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 60/174,612
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(606)
; OTHER INFORMATION: Amino acid sequence of Drosophila Hexosaminidase-1 shown in Fl
; US-09-750-703-4
```

```
Query Match          100.0%; Score 23; DB 10; Length 606;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 NYDA 4
    ||||
Db 475 NYDA 478
```

```
RESULT 29
; US-09-738-626-6180
; Sequence 6180, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
```

APPLICANT: HAVASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENO, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentln ver. 3.0
SEQ ID NO: 6180
LENGTH: 647
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6180

Query Match 100.0%; Score 23; DB 9; Length 647;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 340 NYDA 343

RESULT 30
US-09-969-384-16
Sequence 16, Application US/09969384
Publication No. US20020192749A1
GENERAL INFORMATION:
APPLICANT: Moore, et al.
TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PTO55P1
CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/194,118
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln ver. 2.0
SEQ ID NO: 16
LENGTH: 687
TYPE: PRT
ORGANISM: Homo sapiens
US-09-969-384-16

Query Match 100.0%; Score 23; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 329 NYDA 332

RESULT 31
US-09-969-384-27
Sequence 27, Application US/09969384
Publication No. US20020192749A1
GENERAL INFORMATION:
APPLICANT: Moore, et al.

TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PTO55P1
CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/194,118
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentln ver. 2.0
SEQ ID NO: 27
LENGTH: 687
TYPE: PRT
ORGANISM: Homo sapiens
US-09-969-384-27

Query Match 100.0%; Score 23; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 329 NYDA 332

RESULT 32
US-09-927-180-21
Sequence 21, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 23; DB 10; Length 687;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
DB 546 NYDA 549

RESULT 33
US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match
Best Local Similarity 100.0%; Score 23; DB 10; Length 688;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
DB 547 NYDA 550

RESULT 34
US-09-925-301-1012
Sequence 1012, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1012
LENGTH: 708
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
LOCATION: (18)
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (153)
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (229)
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (433)
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1012

Query Match
Best Local Similarity 100.0%; Score 23; DB 10; Length 708;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
DB 350 NYDA 353

RESULT 35
US-09-738-626-3507
Sequence 3507, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3507
LENGTH: 711
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3507

Query Match
Best Local Similarity 100.0%; Score 23; DB 9; Length 711;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
DB 34 NYDA 37

RESULT 36
US-09-764-868-731

```
; Sequence 731, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT32
; CURRENT APPLICATION NUMBER: US/09/764, 868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 731
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-868-731
```

```
Query Match          100.0%; Score 23; DB 9; Length 721;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
      ||||
Db      405 NYDA 408
```

```
RESULT 37
US-09-738-626-6988
; Sequence 6988, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KETRO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6988
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6988
```

```
Query Match          100.0%; Score 23; DB 9; Length 739;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
      ||||
Db      699 NYDA 702
```

RESULT 38

```
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,784
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2
```

```
Query Match          100.0%; Score 23; DB 10; Length 752;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
      ||||
Db      547 NYDA 550
```

```
RESULT 39
US-09-841-132-386
; Sequence 386, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yashir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 386
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-841-132-386
```

```
Query Match          100.0%; Score 23; DB 10; Length 805;
```

Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||||
Db 7 NYDA 10

RESULT 40

US-09-815-242-12769
; Sequence 12769, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12769
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-09-815-242-12769

Query Match 100.0%; Score 23; DB 10; Length 897;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||||
Db 117 NYDA 120

RESULT 41

US-09-801-368-272
; Sequence 272, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:

; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir

; APPLICANT: Silva, Jeff
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 272
; LENGTH: 904
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae

US-09-801-368-272

Query Match 100.0%; Score 23; DB 10; Length 904;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||||
Db 484 NYDA 487

RESULT 42

US-09-815-242-5836
; Sequence 5836, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5836
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-09-815-242-5836

Query Match 100.0%; Score 23; DB 10; Length 1113;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||||

Db 333 NYDA 336

RESULT 43

US-09-815-242-12447

Sequence 12447, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12447

LENGTH: 1136

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-12447

Query Match

Best Local Similarity 100.0%; Score 23; DB 10; Length 1136;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NYDA 4

Db 110 NYDA 113

RESULT 44

US-09-815-242-12814

Sequence 12814, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12814

LENGTH: 1136

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-12814

Query Match

Best Local Similarity 100.0%; Score 23; DB 10; Length 1136;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NYDA 4

Db 110 NYDA 113

RESULT 45

US-09-815-242-5522

Sequence 5522, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5522

LENGTH: 1179

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-5522

Query Match

Best Local Similarity 100.0%; Score 23; DB 10; Length 1179;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NYDA 4

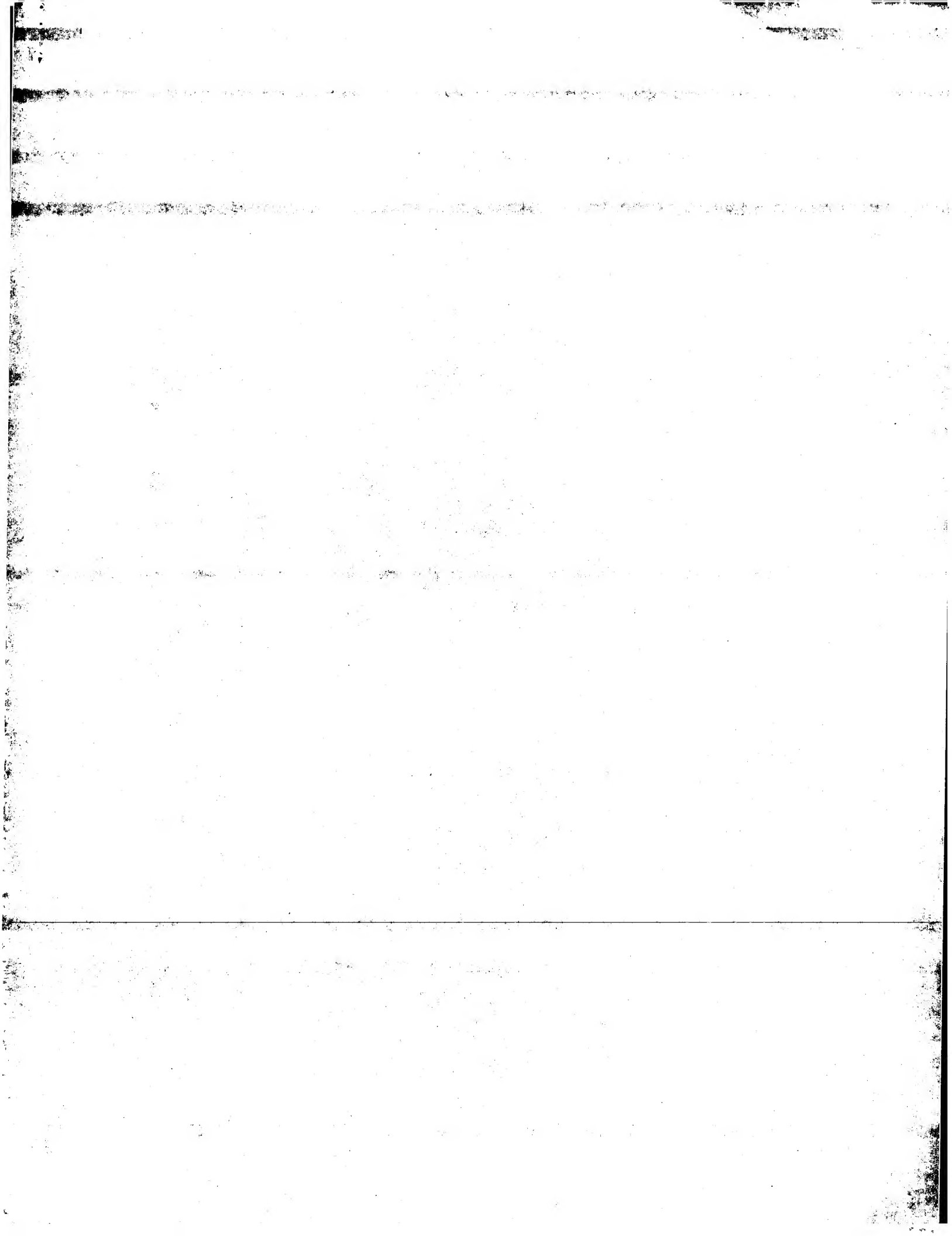
Thu Feb 6 12:30:18 2003

pat943-5.rapb

Page 15

Db 157 NYDA 160

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Job time : 7.83333 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:59 ; Search time 133.167 Seconds
(without alignments)
19.366 Million cell updates/sec

Title: PAT943-5
Perfect score: 23
Sequence: 1 nyda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 1930

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA.Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	100.0	8	25	US-10-145-415-85
2	23	100.0	8	27	US-60-291-149-85
3	23	100.0	11	1	PCR-US99-09466-23
4	23	100.0	11	17	US-09-303-155A-23
5	23	100.0	13	12	US-08-826-516B-164
6	23	100.0	13	12	US-08-826-516-164

7	23	100.0	13	18	US-09-425-679A-8	Sequence 8, Appl
8	23	100.0	13	18	US-09-425-679B-8	Sequence 8, Appl
9	23	100.0	13	18	US-09-425-679C-6	Sequence 6, Appl
10	23	100.0	13	18	US-09-425-679D-6	Sequence 6, Appl
11	23	100.0	13	18	US-09-425-679E-6	Sequence 6, Appl
12	23	100.0	13	25	US-10-116-788A-6	Sequence 6, Appl
13	23	100.0	13	25	US-10-116-788B-6	Sequence 6, Appl
14	23	100.0	13	25	US-10-185-050-164	Sequence 164, Ap
15	23	100.0	17	25	US-10-145-415-64	Sequence 64, Ap
16	23	100.0	17	27	US-60-291-149-64	Sequence 64, Ap
17	23	100.0	19	16	US-09-293-533-6	Sequence 6, Appl
18	23	100.0	19	25	US-10-153-401-6	Sequence 6, Appl
19	23	100.0	26	8	US-08-486-277A-39	Sequence 39, Appl
20	23	100.0	28	22	US-09-864-761-43895	Sequence 43895, A
21	23	100.0	28	25	US-10-182-993-32131	Sequence 32131, A
22	23	100.0	28	26	US-10-203-134-32932	Sequence 32932, A
23	23	100.0	28	26	US-10-203-135-32115	Sequence 32115, A
24	23	100.0	28	26	US-10-203-136-32972	Sequence 32972, A
25	23	100.0	28	26	US-10-203-139-31984	Sequence 31984, A
26	23	100.0	30	16	US-09-270-767-56835	Sequence 56835, A
27	23	100.0	30	16	US-09-270-849B-180383	Sequence 180383, A
28	23	100.0	33	27	US-60-163-233-2412	Sequence 2412, Ap
29	23	100.0	33	27	US-60-163-233-2412	Sequence 2412, Ap
30	23	100.0	36	1	PCR-US01-00663-28914	Sequence 28914, A
31	23	100.0	36	22	US-09-864-761-35859	Sequence 35859, A
32	23	100.0	36	25	US-10-182-993-28071	Sequence 28071, A
33	23	100.0	36	25	US-10-182-993-22331	Sequence 22331, A
34	23	100.0	36	25	US-10-182-997-20978	Sequence 20978, A
35	23	100.0	36	25	US-10-182-998-12622	Sequence 12622, A
36	23	100.0	36	26	US-10-203-134-28641	Sequence 28641, A
37	23	100.0	36	26	US-10-203-135-27555	Sequence 27555, A
38	23	100.0	36	26	US-10-203-136-28648	Sequence 28648, A
39	23	100.0	36	26	US-10-203-137-28914	Sequence 28914, A
40	23	100.0	36	26	US-10-203-138-12929	Sequence 12929, A
41	23	100.0	36	26	US-10-203-139-27174	Sequence 27174, A
42	23	100.0	36	27	US-60-236-359-17638	Sequence 17638, A
43	23	100.0	37	27	US-60-170-373-33932	Sequence 33932, Ap
44	23	100.0	37	27	US-60-195-051-1799	Sequence 1799, Ap
45	23	100.0	38	27	US-60-192-746-1760	Sequence 1760, Ap

ALIGNMENTS

RESULT 1
US-10-145-415-85
; Sequence 85, Application US/10145415
; GENERAL INFORMATION:
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Phillip Eugene
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Enamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Streptomyces tubercidicus
US-10-145-415-85

Query Match 100.0%; Score 23; DB 25; Length 8;
Best Local Similarity 100.0%; Pred. No. 4; 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
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Db 2 NYDA 5

RESULT 2
US-60-291-149-85
; Sequence 85, Application US/60291149
; GENERAL INFORMATION:
; APPLICANT: Ligon, James
; APPLICANT: Pachlatko, J. Paul
; APPLICANT: Hill, D. Steven
; APPLICANT: Molnar, Istvan
; TITLE OF INVENTION: Methods and Compositions for Making Enamectin
; FILE REFERENCE: SYN-010P 109846.126
; CURRENT APPLICATION NUMBER: US/60/291,149
; CURRENT FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 85
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Streptomyces tubercidicus
US-60-291-149-85

Query Match 100.0%; Score 23; DB 27; Length 8;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
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Db 2 NYDA 5

RESULT 3
PCT-US99-09466-23
; Sequence 23, Application PC/TUS9909466A
; GENERAL INFORMATION:
; APPLICANT: Baifu NI
; APPLICANT: Bill N.C. Sun
; APPLICANT: Cecily R.Y. Sun
; TITLE OF INVENTION: G-CSF receptor agonist antibodies and
; FILE REFERENCE: 98-3
; CURRENT APPLICATION NUMBER: PCT/US99/09466A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,575
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: mouse
PCT-US99-09466-23

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
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Db 5 NYDA 8

RESULT 4
US-09-303-155A-23
; Sequence 23, Application US/09303155A
; GENERAL INFORMATION:
; APPLICANT: Baifu NI
; APPLICANT: Bill N.C. Sun
; APPLICANT: Cecily R.Y. Sun
; TITLE OF INVENTION: G-CSF Receptor Agonist Antibodies and

;; TITLE OF INVENTION: Screening Method Therefor
;; FILE REFERENCE: 98-3
;; CURRENT APPLICATION NUMBER: US/09/303,155A
;; CURRENT FILING DATE: 1999-04-30
;; PRIOR APPLICATION NUMBER: 60/083,575
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 23
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: mouse
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QY 1 NYDA 4
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Db 5 NYDA 8

RESULT 5
US-08-826-516B-164
; Sequence 164, Application US/08826516B
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; NUMBER OF SEQUENCES: 230
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennile & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516B
; FILING DATE: 03-Apr-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-826-516B-164

Query Match 100.0%; Score 23; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
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Db 7 NYDA 10

RESULT 6
US-08-826-516-164
; Sequence 164, Application US/08826516D
; GENERAL INFORMATION:
; APPLICANT: Pflorzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516D
; FILING DATE: 03-Apr-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8664/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; STRANDEDNESS: <unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-08-826-516-164
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
Db 7 NYDA 10
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US-09-425-679A-8
; Sequence 8, Application US/09425679A
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Weber, Annika
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: Colostrum SAA
; CURRENT APPLICATION NUMBER: US/09/425,679A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Equine
US-09-425-679A-8
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Best Local Similarity 100.0%; Pred. No. 2e+02;
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Db 2 NYDA 5
RESULT 8
US-09-425-679B-8
; Sequence 8, Application US/09425679B
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Weber, Annika
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: Colostrum SAA
; CURRENT APPLICATION NUMBER: US/09/425,679B
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Equine
US-09-425-679B-8
Query Match 100.0%; Score 23; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
Db 2 NYDA 5
RESULT 9
US-09-425-679C-6
; Sequence 6, Application US/09425679C
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Nebraska Medical Center
; APPLICANT: McDonald, Thomas
; APPLICANT: Weber, Annika
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: UNMC 63142
; CURRENT APPLICATION NUMBER: US/09/425,679C
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,611
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-425-679C-6
Query Match 100.0%; Score 23; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
Db 2 NYDA 5
RESULT 10
US-09-425-679D-6
; Sequence 6, Application US/09425679D
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Weber, Annika L.
US-09-425-679A-8

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; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: UNMC 63142
; CURRENT APPLICATION NUMBER: US/09/425,679D
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,611
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-425-679D-6
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Query Match          100.0%; Score 23; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       2 NYDA 5
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RESULT 11
US-09-425-679E-6
; Sequence 6, Application US/09425679E
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Weber, Annika L.
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: UNMC 63142
; CURRENT APPLICATION NUMBER: US/09/425,679E
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,611
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-425-679E-6
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Query Match          100.0%; Score 23; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 NYDA 4
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Db       2 NYDA 5
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RESULT 12
US-10-116-788A-6
; Sequence 6, Application US/10116788A
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Larson, Marilyn A.
; APPLICANT: Weber, Annika
; TITLE OF INVENTION: Genomic Mammary Amyloid A Sequence
; FILE REFERENCE: P04557US1
; CURRENT APPLICATION NUMBER: US/10/116,788A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/425,679
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/218,611
; PRIOR FILING DATE: 2000-07-17
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; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-116-788A-6
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 NYDA 4
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Db       2 NYDA 5
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RESULT 13
US-10-116-788B-6
; Sequence 6, Application US/10116788B
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Nebraska Medical Center
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Larson, Marilyn A.
; APPLICANT: Weber, Annika
; TITLE OF INVENTION: Genomic Mammary Amyloid A Sequence
; FILE REFERENCE: P04557US1
; CURRENT APPLICATION NUMBER: US/10/116,788B
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/425,679
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/218,611
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-116-788B-6
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Query Match          100.0%; Score 23; DB 25; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 NYDA 4
        ||||
Db       2 NYDA 5
```

```
RESULT 14
US-10-185-050-164
; Sequence 164, Application US/10185050
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA: US/10/185,030
: APPLICATION NUMBER: US/10/185,030
: FILING DATE: 28-Jun-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/826,516
: FILING DATE: 03-Apr-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: MISROCK, S. LESLIE
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 1101-208-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 896-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 164:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-10-185-050-164

Query Match      100.0%; Score 23; DB 25; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NYDA 4
        ||||
Db      7 NYDA 10

RESULT 15
US-10-145-415-64
: Sequence 64, Application US/10145415
: GENERAL INFORMATION:
: APPLICANT: Buckel, Thomas Gunter
: APPLICANT: Hammer, Philip Eugene
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ligon, James Madison
: APPLICANT: Molnar, Istvan
: APPLICANT: Pachlatko, Johannes Paul
: APPLICANT: Zirkle, Ross Eric
: TITLE OF INVENTION: Methods and Compositions for Making Emamectin
: FILE REFERENCE: SYN-117 109846.312
: CURRENT APPLICATION NUMBER: US/10/145,415
: CURRENT FILING DATE: 2002-05-14
: PRIOR APPLICATION NUMBER: US 60/291,149
: PRIOR FILING DATE: 2001-05-16
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 64
: LENGTH: 17
: TYPE: PRT
: ORGANISM: Streptomyces tubercidicus
US-10-145-415-64

Query Match      100.0%; Score 23; DB 25; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NYDA 4
        ||||
Db      9 NYDA 12

RESULT 16
US-60-291-149-64
: Sequence 64, Application US/60291149
: GENERAL INFORMATION:
```

```

: APPLICANT: Ligon, James
: APPLICANT: Pachlatko, J. Paul
: APPLICANT: Hill, D. Steven
: APPLICANT: Molnar, Istvan
: TITLE OF INVENTION: Methods and Compositions for Making Emamectin
: FILE REFERENCE: SYN-010P 109846.126
: CURRENT APPLICATION NUMBER: US/60/291,149
: CURRENT FILING DATE: 2001-05-16
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 64
: LENGTH: 17
: TYPE: PRT
: ORGANISM: Streptomyces tubercidicus
US-60-291-149-64

Query Match      100.0%; Score 23; DB 27; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NYDA 4
        ||||
Db      9 NYDA 12

RESULT 17
US-09-293-533-6
: Sequence 6, Application US/09293533
: GENERAL INFORMATION:
: APPLICANT: Chatterjee, Malaya
: APPLICANT: Poon, Kenneth A.
: APPLICANT: Chatterjee, Sunil K.
: TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
: TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/293,533
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION:
: APPLICATION NUMBER: US/08/752,844
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Schiff, J. Michael
: REGISTRATION NUMBER: 40,253
: REFERENCE/DOCKET NUMBER: 30414-20002.21
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 19 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-293-533-6

Query Match      100.0%; Score 23; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 NYDA 4
| | | |
Db 2 NYDA 5

RESULT 18
US-10-153-401-6
Sequence 6, Application US/10153401
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Roon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-153-401-6

Query Match 100.0%; Score 23; DB 25; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
Db 2 NYDA 5

RESULT 19
US-08-486-277A-39
Sequence 39, Application US/08486277A
GENERAL INFORMATION:
APPLICANT: Heinemann Ph.D., Stephen F.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Hollmann Ph.D., Michael
APPLICANT: Bettler Ph.D., Bernhard

APPLICANT: Jensen Ph.D., Jan E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,277A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9987
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-1995
TELEFAX: (619) 546-9392
TELEX:
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-486-277A-39

Query Match 100.0%; Score 23; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
Db 1 NYDA 4

RESULT 20
US-09-864-761-43895
Sequence 43895, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43895
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.43
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
US-09-864-761-43895

Query Match
Best Local Similarity 100.0%; Score 23; DB 22; Length 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
|||||
Db 7 NYDA 10

RESULT 21
US-10-182-993-32131
Sequence 32131, Application US/10182993
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN
FILE REFERENCE: PB 0004 WO 2
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US/10/182,993
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 37811
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 32131
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
US-10-182-993-32131

Query Match
Best Local Similarity 100.0%; Score 23; DB 25; Length 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
|||||
Db 7 NYDA 10

RESULT 22
US-10-203-134-32932
Sequence 32932, Application US/10203134
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW
FILE REFERENCE: PB 0004 WO 6
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US/10/203,134
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38628
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 32932
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
US-10-203-134-32932

Query Match
Best Local Similarity 100.0%; Score 23; DB 26; Length 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
|||||
Db 7 NYDA 10

RESULT 23
US-10-203-135-32115

```
Sequence 32115, Application US/10203135
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 5
CURRENT APPLICATION NUMBER: US/10/203,135
PRIORITY FILING DATE: 2002-08-02
PRIORITY FILING DATE: 04 February 2000 (04.02.00)
PRIORITY FILING DATE: 26 May 2000 (26.05.00)
PRIORITY FILING DATE: 03 August 2000 (03.08.00)
PRIORITY FILING DATE: 03 October 2000 (03.10.00)
PRIORITY FILING DATE: 27 September 2000 (27.09.00)
PRIORITY FILING DATE: 21 September 2000 (21.09.00)
PRIORITY FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 37012
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 32115
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48
US-10-203-135-32115

Query Match
Best Local Similarity 100.0%; Score 23; DB 26; Length 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 7 NYDA 10

RESULT 24
US-10-203-136-32972
Sequence 32972, Application US/10203136
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 3
CURRENT APPLICATION NUMBER: US/10/203,136
PRIORITY FILING DATE: 2002-08-02
PRIORITY FILING DATE: 04 February 2000 (04.02.00)
PRIORITY FILING DATE: 26 May 2000 (26.05.00)
PRIORITY FILING DATE: 03 August 2000 (03.08.00)
PRIORITY FILING DATE: 03 October 2000 (03.10.00)
PRIORITY FILING DATE: 27 September 2000 (27.09.00)
PRIORITY FILING DATE: 21 September 2000 (21.09.00)
PRIORITY FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 37156
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 31984
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
US-10-203-136-31984

Query Match
Best Local Similarity 100.0%; Score 23; DB 26; Length 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 7 NYDA 10

RESULT 26
```

```
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38578
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 32972
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.43
US-10-203-136-32972

Query Match
Best Local Similarity 100.0%; Score 23; DB 26; Length 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 7 NYDA 10
```

```
RESULT 25
US-10-203-139-31984
Sequence 31984, Application US/10203139
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: PB 0004 WO 4
CURRENT APPLICATION NUMBER: US/10/203,139
PRIORITY FILING DATE: 2002-08-02
PRIORITY FILING DATE: 04 February 2000 (04.02.00)
PRIORITY FILING DATE: 26 May 2000 (26.05.00)
PRIORITY FILING DATE: 03 August 2000 (03.08.00)
PRIORITY FILING DATE: 03 October 2000 (03.10.00)
PRIORITY FILING DATE: 27 September 2000 (27.09.00)
PRIORITY FILING DATE: 21 September 2000 (21.09.00)
PRIORITY FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 37156
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 31984
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
US-10-203-139-31984

Query Match
Best Local Similarity 100.0%; Score 23; DB 26; Length 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 7 NYDA 10

RESULT 26
```

US-09-270-767-56835
; Sequence 56835, Application US/09270767
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56835
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56835

Query Match
Best Local Similarity 100.0%; Score 23; DB 16; Length 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
Db 8 NYDA 11

RESULT 27
US-09-270-8498-180383
; Sequence 180383, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180383
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-8498-180383

Query Match
Best Local Similarity 100.0%; Score 23; DB 16; Length 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
Db 8 NYDA 11

RESULT 28
US-60-163-233-2412
; Sequence 2412, Application US/60163233
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
; FILE REFERENCE: CLO00133
; CURRENT APPLICATION NUMBER: US/60/163,233
; CURRENT FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 4426
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2412
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human
US-60-163-233-2412

Query Match 100.0%; Score 23; DB 27; Length 33;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
Db 12 NYDA 15

RESULT 29
US-60-169-867-6162
; Sequence 6162, Application US/60169867
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
; FILE REFERENCE: CLO00160
; CURRENT APPLICATION NUMBER: US/60/169,867
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 8230
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6162
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Human
US-60-169-867-6162

Query Match
Best Local Similarity 100.0%; Score 23; DB 27; Length 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
Db 12 NYDA 15

RESULT 30
PCT-US01-00663-28914
; Sequence 28914, Application PC/TUS0100663
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: PCT/US01/00663
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24253.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 28914
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4

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; OTHER INFORMATION: EST_HUMAN HIT: AM403965.1, EVALUE 2.00e-13
PCT-US01-00663-28914
Query Match          100.0%; Score 23; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYDA 4
    ||||
Db 30 NYDA 33

RESULT 31
US-09-864-761-35859
; Sequence 35859, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmiga-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35859
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
```

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; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EST_HUMAN HIT: AM403965.1, EVALUE 2.00e-13
US-09-864-761-35859
Query Match          100.0%; Score 23; DB 22; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYDA 4
    ||||
Db 30 NYDA 33

RESULT 32
US-10-182-993-28071
; Sequence 28071, Application US/10182993
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: PB 0004 WO 2
; CURRENT APPLICATION NUMBER: US/10/182,993
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37811
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 28071
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
US-10-182-993-28071
Query Match          100.0%; Score 23; DB 25; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYDA 4
    ||||
Db 30 NYDA 33

RESULT 33
US-10-182-995-22331
; Sequence 22331, Application US/10182995
; GENERAL INFORMATION:
```



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: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Hanzel, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: PB 0004 WO 1
: CURRENT APPLICATION NUMBER: US/10/182,995
: CURRENT FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 29119
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 22331
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC010732.1
: FEATURE:
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
: FEATURE:
: OTHER INFORMATION: EST_HUMAN HIT: AM403965.1, EVALUUE 2.00e-13
: US-10-182-995-22331

Query Match
Best Local Similarity 100.0%; Score 23; DB 25; Length 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYDA 4
    ||||
Db 30 NYDA 33

RESULT 34
: US-10-182-997-20978
: Sequence 20978, Application US/10182997
: GENERAL INFORMATION:
: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Hanzel, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: PB 0004 WO 10
: CURRENT APPLICATION NUMBER: US/10/182,997
: CURRENT FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 15009
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 12622
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC010732.1
: FEATURE:
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 15
: FEATURE:
: OTHER INFORMATION: EST_HUMAN HIT: AM403965.1, EVALUUE 2.00e-13
: US-10-182-998-12622

Query Match
Best Local Similarity 100.0%; Score 23; DB 25; Length 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYDA 4
    ||||
Db 30 NYDA 33
```

```

: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 26941
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 20978
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC010732.1
: FEATURE:
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9
: FEATURE:
: OTHER INFORMATION: EST_HUMAN HIT: AM403965.1, EVALUUE 2.00e-13
: US-10-182-997-20978

Query Match
Best Local Similarity 100.0%; Score 23; DB 25; Length 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYDA 4
    ||||
Db 30 NYDA 33

RESULT 35
: US-10-182-998-12622
: Sequence 12622, Application US/10182998
: GENERAL INFORMATION:
: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Hanzel, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
: FILE REFERENCE: PB 0004 WO 9
: CURRENT APPLICATION NUMBER: US/10/182,998
: CURRENT FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 15009
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 12622
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC010732.1
: FEATURE:
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 15
: FEATURE:
: OTHER INFORMATION: EST_HUMAN HIT: AM403965.1, EVALUUE 2.00e-13
: US-10-182-998-12622

Query Match
Best Local Similarity 100.0%; Score 23; DB 25; Length 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYDA 4
    ||||
Db 30 NYDA 33
```

Db 30 NYDA 33

RESULT 36
US-10-203-134-28641
; Sequence 28641, Application US/10203134
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 6
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/203,134
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38628
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 28641
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW403965.1, EVALU 2.00e-13
US-10-203-134-28641

Query Match 100.0%; Score 23; DB 26; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 30 NYDA 33

RESULT 37
US-10-203-135-27555
; Sequence 27555, Application US/10203135
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 5
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/203,135
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37012
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 27555
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.4
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW403965.1, EVALU 2.00e-13
US-10-203-135-27555

Query Match 100.0%; Score 23; DB 26; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
Db 30 NYDA 33

RESULT 38
US-10-203-136-28648
; Sequence 28648, Application US/10203136
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 3
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/203,136
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38578
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 28648
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW403965.1, EVALU 2.00e-13
US-10-203-136-28648

```
Query Match          100.0%; Score 23; DB 26; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
       |||||
Db      30 NYDA 33

RESULT 39
US-10-203-137-28914
; Sequence 28914, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 28914
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: EST_HUMAN HIT: AW403965.1, EVALUATE 2.00e-13
US-10-203-137-28914

Query Match          100.0%; Score 23; DB 26; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
       |||||
Db      30 NYDA 33

RESULT 40
US-10-203-138-12929
; Sequence 12929, Application US/10203138
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
```

```
; CURRENT APPLICATION NUMBER: US/10/203,138
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 12929
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010732.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
; TITLE OF INVENTION: EST_HUMAN HIT: AW403965.1, EVALUATE 2.00e-13
US-10-203-138-12929

Query Match          100.0%; Score 23; DB 26; Length 36;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
       |||||
Db      30 NYDA 33

RESULT 41
US-10-203-139-27774
; Sequence 27774, Application US/10203139
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
; FILE REFERENCE: PB 0004 WO 4
; CURRENT APPLICATION NUMBER: US/10/203,139
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37156
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 27774
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
FEATURE:
OTHER INFORMATION: MAP TO AC010732.1
FEATURE:
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
FEATURE:
OTHER INFORMATION: EST_HUMAN HIT: AM403965.1, EVALUO 2.00e-13
US-10-203-139-27774
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 26; Length 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 30 NYDA 33
```

RESULT 42

```
US-60-236-359-17638
Sequence 17638, Application US/60236359
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: MDHMOF-4P
CURRENT APPLICATION NUMBER: US/60/236,359
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 21709
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 17638
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010732.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 15
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
OTHER INFORMATION: EST_HUMAN HIT: BE336641.1, EVALUO 2.00e-13
US-60-236-359-17638
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 27; Length 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 30 NYDA 33
```

RESULT 43

```
US-60-170-373-3392
Sequence 3392, Application US/60170373
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
FILE REFERENCE: CL000149
CURRENT APPLICATION NUMBER: US/60/170,373
CURRENT FILING DATE: 1999-12-13
```

```
NUMBER OF SEQ ID NOS: 4282
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3392
LENGTH: 37
TYPE: PRT
ORGANISM: Human
US-60-170-373-3392
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 27; Length 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 28 NYDA 31
```

RESULT 44

```
US-60-195-053-1799
Sequence 1799, Application US/60195053
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
FILE REFERENCE: CL000427
CURRENT APPLICATION NUMBER: US/60/195,053
CURRENT FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 2836
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1799
LENGTH: 37
TYPE: PRT
ORGANISM: HUMAN
US-60-195-053-1799
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 27; Length 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 21 NYDA 24
```

RESULT 45

```
US-60-192-746-1760
Sequence 1760, Application US/60192746
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CL000401
CURRENT APPLICATION NUMBER: US/60/192,746
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 2142
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1760
LENGTH: 38
TYPE: PRT
ORGANISM: HUMAN
US-60-192-746-1760
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 27; Length 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 25 NYDA 28
```

Thu Feb 6 12:30:19 2003

pat943-5.rapm

Page 15

Search completed: February 6, 2003, 11:37:36
Job time : 135.167 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:19:49 ; Search time 14 Seconds
(without alignments)
23.165 Million cell updates/sec

Title: PAT943-5
Perfect score: 23
Sequence: 1 nyda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 363

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_MA_New:*
1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	23	100.0	36	6	US-10-203-138A-12929
2	23	100.0	45	6	US-10-099-782A-43
3	23	100.0	46	6	US-10-099-782A-44
4	23	100.0	47	6	US-10-099-782A-45
5	23	100.0	48	6	US-10-099-782A-46
6	23	100.0	49	6	US-10-099-782A-47
7	23	100.0	50	6	US-10-099-782A-48
8	23	100.0	51	6	US-10-099-782A-49
9	23	100.0	52	6	US-10-099-782A-50
10	23	100.0	53	6	US-10-099-782A-51
11	23	100.0	54	6	US-10-099-782A-52
12	23	100.0	55	6	US-10-099-782A-53
13	23	100.0	56	6	US-10-099-782A-54
14	23	100.0	57	6	US-10-099-782A-55
15	23	100.0	58	6	US-10-099-782A-56
16	23	100.0	59	6	US-10-099-782A-57
17	23	100.0	60	6	US-10-099-782A-58
18	23	100.0	61	6	US-10-099-782A-59
19	23	100.0	62	6	US-10-099-782A-60
20	23	100.0	63	6	US-10-099-782A-61
21	23	100.0	64	6	US-10-099-782A-62
22	23	100.0	64	6	US-10-099-782A-141
23	23	100.0	64	6	US-10-099-782A-241
24	23	100.0	65	6	US-10-099-782A-140
25	23	100.0	65	6	US-10-099-782A-240
26	23	100.0	66	5	US-09-084-303B-291

27	23	100.0	66	6	US-10-099-782A-63	Sequence 63, App1
28	23	100.0	66	6	US-10-099-782A-139	Sequence 139, App
29	23	100.0	66	6	US-10-099-782A-239	Sequence 239, App
30	23	100.0	66	6	US-10-338-740-291	Sequence 291, App
31	23	100.0	67	6	US-10-099-782A-64	Sequence 64, App1
32	23	100.0	67	6	US-10-099-782A-138	Sequence 138, App
33	23	100.0	67	6	US-10-099-782A-238	Sequence 238, App
34	23	100.0	68	6	US-10-099-782A-65	Sequence 65, App1
35	23	100.0	68	6	US-10-099-782A-137	Sequence 137, App
36	23	100.0	68	6	US-10-099-782A-237	Sequence 237, App
37	23	100.0	69	6	US-10-099-782A-66	Sequence 66, App1
38	23	100.0	69	6	US-10-099-782A-136	Sequence 136, App
39	23	100.0	69	6	US-10-099-782A-236	Sequence 236, App
40	23	100.0	70	6	US-10-099-782A-67	Sequence 67, App1
41	23	100.0	70	6	US-10-099-782A-135	Sequence 135, App
42	23	100.0	70	6	US-10-099-782A-235	Sequence 235, App
43	23	100.0	71	6	US-10-099-782A-68	Sequence 68, App1
44	23	100.0	71	6	US-10-099-782A-133	Sequence 133, App
45	23	100.0	71	6	US-10-099-782A-234	Sequence 234, App

ALIGNMENTS

RESULT 1
US-10-203-138A-12929
Sequence 12929, Application US/10203138A
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,365
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 15438
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 12929
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010732.1
FEATURE:
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
OTHER INFORMATION: EST_HUMAN HIT: AW403965.1, EVALUATE 2.00e-13
US-10-203-138A-12929
Query Match 100.0%; Score 23; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NYDA 4
DB 30 NYDA 33

```
RESULT 2
US-10-099-782A-43
; Sequence 43, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-43
```

```
Query Match          100.0%; Score 23; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45

RESULT 3
US-10-099-782A-44
; Sequence 44, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-44
```

```
Query Match          100.0%; Score 23; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45

RESULT 4
US-10-099-782A-45
; Sequence 45, Application US/10099782A
```

```
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-45
```

```
Query Match          100.0%; Score 23; DB 6; Length 47;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45

RESULT 5
US-10-099-782A-46
; Sequence 46, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-46
```

```
Query Match          100.0%; Score 23; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45

RESULT 6
US-10-099-782A-47
; Sequence 47, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
```



```
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-47
```

```
Query Match          100.0%; Score 23; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 7
US-10-099-782A-48
; Sequence 48, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-48
```

```
Query Match          100.0%; Score 23; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 8
US-10-099-782A-49
; Sequence 49, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
```

```
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-49
```

```
Query Match          100.0%; Score 23; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 9
US-10-099-782A-50
; Sequence 50, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-50
```

```
Query Match          100.0%; Score 23; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 10
US-10-099-782A-51
; Sequence 51, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-51
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 11
; Sequence 52, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-52
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 54;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 12
; Sequence 53, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo Sapiens
```

```
US-10-099-782A-53
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 13
; Sequence 54, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-54
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NYDA 4
    ||||
Db 42 NYDA 45
```

```
RESULT 14
; Sequence 55, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-55
```

```
Query Match
Best Local Similarity 100.0%; Score 23; DB 6; Length 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 NYDA 4
||||
Db 42 NYDA 45

RESULT 15

US-10-099-782A-56
; Sequence 56, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-56

Query Match 100.0%; Score 23; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 42 NYDA 45

RESULT 16

US-10-099-782A-57
; Sequence 57, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-57

Query Match 100.0%; Score 23; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 42 NYDA 45

RESULT 17

US-10-099-782A-58
; Sequence 58, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-58

Query Match 100.0%; Score 23; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 42 NYDA 45

RESULT 18

US-10-099-782A-59
; Sequence 59, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-59

Query Match 100.0%; Score 23; DB 6; Length 61;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 42 NYDA 45

RESULT 19

US-10-099-782A-60
; Sequence 60, Application US/10099782A
; GENERAL INFORMATION:

```
APPLICANT: Ji-Ming Wang
APPLICANT: Joost J. Oppenheim
APPLICANT: Shao-Bo Su
APPLICANT: Wang-Hua Gong
APPLICANT: Ji-Liang Gao
APPLICANT: Philip M. Murphy
TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
RECEPTOR BY SERUM AMYLOID A (SAA)
FILE REFERENCE: NIH173.001C1
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: PCT/US99/21770
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 62
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-099-782A-60
```

```
Query Match          100.0%; Score 23; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
      ||||
DB      42 NYDA 45
```

```
RESULT 20
US-10-099-782A-61
; Sequence 61, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-61
```

```
Query Match          100.0%; Score 23; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
      ||||
DB      42 NYDA 45
```

```
RESULT 21
US-10-099-782A-62
; Sequence 62, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
```

```
APPLICANT: Philip M. Murphy
APPLICANT: Joost J. Oppenheim
APPLICANT: Shao-Bo Su
APPLICANT: Wang-Hua Gong
APPLICANT: Ji-Liang Gao
APPLICANT: Philip M. Murphy
TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
RECEPTOR BY SERUM AMYLOID A (SAA)
FILE REFERENCE: NIH173.001C1
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: PCT/US99/21770
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 62
LENGTH: 64
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-099-782A-62
```

```
Query Match          100.0%; Score 23; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
      ||||
DB      42 NYDA 45
```

```
RESULT 22
US-10-099-782A-141
; Sequence 141, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-141
```

```
Query Match          100.0%; Score 23; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NYDA 4
      ||||
DB      42 NYDA 45
```

```
RESULT 23
US-10-099-782A-241
; Sequence 241, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099/782A
```

```
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-241
```

```
Query Match          100.0%; Score 23; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    |||
Db 1 NYDA 4
```

```
RESULT 24
US-10-099-782A-140
; Sequence 140, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-140
```

```
Query Match          100.0%; Score 23; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    |||
Db 2 NYDA 5
```

```
RESULT 25
US-10-099-782A-240
; Sequence 240, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FASTSEQ for Windows Version 4.0
```

```
; SEQ ID NO 240
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-240
```

```
Query Match          100.0%; Score 23; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    |||
Db 2 NYDA 5
```

```
RESULT 26
US-09-084-303B-291
; Sequence 291, Application US/09084303B
; GENERAL INFORMATION:
; APPLICANT: Dobershtein, Stephen
; APPLICANT: Reddy, Bindu
; APPLICANT: Platt, Darren
; APPLICANT: Ferguson, Kimberly
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AN
; TITLE OF INVENTION: THERAPE
; FILE REFERENCE: 7326-069-999
; CURRENT APPLICATION NUMBER: US/09/084,303B
; CURRENT FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 291
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa = any amino acid
US-09-084-303B-291
```

```
Query Match          100.0%; Score 23; DB 5; Length 66;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    |||
Db 63 NYDA 66
```

```
RESULT 27
US-10-099-782A-63
; Sequence 63, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-63
```

Query Match 100.0%; Score 23; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 42 NYDA 45

RESULT 28
 US-10-099-782A-139
 ; Sequence 139, Application US/10099782A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ji-Ming Wang
 ; APPLICANT: Joost J. Oppenheim
 ; APPLICANT: Shao-Bo Su
 ; APPLICANT: Wang-Hua Gong
 ; APPLICANT: Ji-Liang Gao
 ; APPLICANT: Philip M. Murphy
 ; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
 ; FILE REFERENCE: NIH173.001C1
 ; CURRENT APPLICATION NUMBER: US/10/099,782A
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/21770
 ; NUMBER OF SEQ ID NOS: 301
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 139
 ; LENGTH: 66
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-099-782A-139

Query Match 100.0%; Score 23; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 3 NYDA 6

RESULT 29
 US-10-099-782A-239
 ; Sequence 239, Application US/10099782A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ji-Ming Wang
 ; APPLICANT: Joost J. Oppenheim
 ; APPLICANT: Shao-Bo Su
 ; APPLICANT: Wang-Hua Gong
 ; APPLICANT: Ji-Liang Gao
 ; APPLICANT: Philip M. Murphy
 ; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
 ; FILE REFERENCE: NIH173.001C1
 ; CURRENT APPLICATION NUMBER: US/10/099,782A
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/21770
 ; NUMBER OF SEQ ID NOS: 301
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 239
 ; LENGTH: 66
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-099-782A-239

Query Match 100.0%; Score 23; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 3 NYDA 6

RESULT 30
 US-10-339-740-291
 ; Sequence 291, Application US/10339740
 ; GENERAL INFORMATION:
 ; APPLICANT: Doberstein, Stephen
 ; APPLICANT: Reddy, Bindu
 ; APPLICANT: Platt, Darren
 ; APPLICANT: Ferguson, Kimberly
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AN
 ; FILE REFERENCE: 7326-069-999
 ; CURRENT APPLICATION NUMBER: US/10/339,740
 ; PRIOR FILING DATE: 2003-01-09
 ; PRIOR APPLICATION NUMBER: US/09/084,303A
 ; NUMBER OF SEQ ID NOS: 298
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 291
 ; LENGTH: 66
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: misc-feature
 ; LOCATION: (1)..(30)
 ; OTHER INFORMATION: Xaa = any amino acid
 US-10-339-740-291

Query Match 100.0%; Score 23; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 63 NYDA 66

RESULT 31
 US-10-099-782A-64
 ; Sequence 64, Application US/10099782A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ji-Ming Wang
 ; APPLICANT: Joost J. Oppenheim
 ; APPLICANT: Shao-Bo Su
 ; APPLICANT: Wang-Hua Gong
 ; APPLICANT: Ji-Liang Gao
 ; APPLICANT: Philip M. Murphy
 ; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
 ; FILE REFERENCE: NIH173.001C1
 ; CURRENT APPLICATION NUMBER: US/10/099,782A
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/21770
 ; NUMBER OF SEQ ID NOS: 301
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 64
 ; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-099-782A-64

Query Match 100.0%; Score 23; DB 6; Length 67;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 42 NYDA 45

```

RESULT 32
US-10-099-782A-138
; Sequence 138, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-138

```

```

Query Match          100.0%; Score 23; DB 6; Length 67;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
Db 4 NYDA 7

```

```

RESULT 33
US-10-099-782A-238
; Sequence 238, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-238

```

```

Query Match          100.0%; Score 23; DB 6; Length 67;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
Db 4 NYDA 7

```

```

RESULT 34
US-10-099-782A-65
; Sequence 65, Application US/10099782A

```

```

; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-65

```

```

Query Match          100.0%; Score 23; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
Db 42 NYDA 45

```

```

RESULT 35
US-10-099-782A-137
; Sequence 137, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-137

```

```

Query Match          100.0%; Score 23; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
Db 5 NYDA 8

```

```

RESULT 36
US-10-099-782A-237
; Sequence 237, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong

```

```

; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 68
; TYPE: PRN
; ORGANISM: Homo Sapiens
US-10-099-782A-237

```

```

Query Match          100.0%; Score 23; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
DB 5 NYDA 8

```

```

RESULT 37
US-10-099-782A-66
; Sequence 66, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 69
; TYPE: PRN
; ORGANISM: Homo Sapiens
US-10-099-782A-66

```

```

Query Match          100.0%; Score 23; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
DB 42 NYDA 45

```

```

RESULT 38
US-10-099-782A-136
; Sequence 136, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1

```

```

; CURRENT APPLICATION NUMBER: US/10/099,782A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 69
; TYPE: PRN
; ORGANISM: Homo Sapiens
US-10-099-782A-136

```

```

Query Match          100.0%; Score 23; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
DB 6 NYDA 9

```

```

RESULT 39
US-10-099-782A-236
; Sequence 236, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 69
; TYPE: PRN
; ORGANISM: Homo Sapiens
US-10-099-782A-236

```

```

Query Match          100.0%; Score 23; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NYDA 4
    ||||
DB 6 NYDA 9

```

```

RESULT 40
US-10-099-782A-67
; Sequence 67, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301

```



```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-67
```

```
Query Match          100.0%; Score 23; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
DB 42 NYDA 45
```

```
RESULT 41
US-10-099-782A-135
; Sequence 135, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-135
```

```
Query Match          100.0%; Score 23; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
DB 7 NYDA 10
```

```
RESULT 42
US-10-099-782A-235
; Sequence 235, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo Sapiens
```

```
US-10-099-782A-235
```

```
Query Match          100.0%; Score 23; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
DB 7 NYDA 10
```

```
RESULT 43
US-10-099-782A-68
; Sequence 68, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-68
```

```
Query Match          100.0%; Score 23; DB 6; Length 71;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NYDA 4
    ||||
DB 42 NYDA 45
```

```
RESULT 44
US-10-099-782A-133
; Sequence 133, Application US/10099782A
; GENERAL INFORMATION:
; APPLICANT: Ji-Ming Wang
; APPLICANT: Joost J. Oppenheim
; APPLICANT: Shao-Bo Su
; APPLICANT: Wang-Hua Gong
; APPLICANT: Ji-Liang Gao
; APPLICANT: Philip M. Murphy
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL
; FILE REFERENCE: NIH173.001C1
; CURRENT APPLICATION NUMBER: US/10/099,782A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US99/21770
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-099-782A-133
```

```
Query Match          100.0%; Score 23; DB 6; Length 71;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 NYDA 4
 Db 9 NYDA 12

RESULT 45
 US-10-099-782A-134
 : Sequence 134. Application US/10099782A
 : GENERAL INFORMATION:
 : APPLICANT: Ji-Ming Wang
 : APPLICANT: Joost J. Oppenheim
 : APPLICANT: Shao-Bo Su
 : APPLICANT: Wang-Hua Gong
 : APPLICANT: Ji-Liang Gao
 : APPLICANT: Philip M. Murphy
 : TITLE OF INVENTION: UTILIZATION OF PPRL AS A FUNCTIONAL
 : FILE REFERENCE: NIH173.001C1
 : CURRENT APPLICATION NUMBER: US/10/099,782A
 : CURRENT FILING DATE: 2002-10-25
 : PRIOR APPLICATION NUMBER: PCT/US99/21770
 : PRIOR FILING DATE: 1999-09-22
 : NUMBER OF SEQ ID NOS: 301
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 134
 : LENGTH: 71
 : TYPE: PRT
 : ORGANISM: Homo Sapiens
 US-10-099-782A-134

Query Match 100.0%; Score 23; DB 6; Length 71;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 Db 8 NYDA 11

Search completed: February 6, 2003, 11:39:04
 Job time : 15 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 : Search time 10.5 Seconds
(without alignments)
36.623 Million cell updates/sec

Title: PAT943-5

Perfect score: 23

Sequence: 1 nyda 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR-73:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	64	1 YLMNA	amyloid protein AA
2	23	100.0	76	1 YLMQAR	amyloid protein AA
3	23	100.0	80	1 YLMDA	amyloid protein AA
4	23	100.0	80	2 I59148	apoliipoprotein B -
5	23	100.0	83	2 I71951	serum amyloid A -
6	23	100.0	85	2 F97131	hypothetical prote
7	23	100.0	90	1 YLCTA	amyloid protein AA
8	23	100.0	90	1 A60952	amyloid protein AA
9	23	100.0	90	1 S60667	phosphotransferase
10	23	100.0	91	2 I71950	serum amyloid A -
11	23	100.0	94	1 R5YM23	ribosomal protein
12	23	100.0	100	2 AE1789	hypothetical prote
13	23	100.0	103	2 S06386	serum amyloid A pr
14	23	100.0	106	2 A27227	amyloid protein A
15	23	100.0	106	2 AF1413	hypothetical prote
16	23	100.0	108	2 B40085	ubiquitin carboxyl
17	23	100.0	108	2 B82863	hypothetical prote
18	23	100.0	109	2 B38645	amyloid A-like pro
19	23	100.0	110	2 S26333	Ig heavy chain V r
20	23	100.0	110	2 A28573	serum amyloid A pr
21	23	100.0	110	2 T27515	hypothetical prote
22	23	100.0	112	2 AG1646	hypothetical prote
23	23	100.0	116	2 D38645	amyloid A protein
24	23	100.0	116	2 E38645	amyloid A protein
25	23	100.0	119	1 YLUGA	amyloid protein AA
26	23	100.0	119	2 H84991	hypothetical prote
27	23	100.0	121	2 C38645	amyloid A protein
28	23	100.0	122	1 YLHUS	serum amyloid A1 p
29	23	100.0	122	1 YLHUA	serum amyloid A2 p

30	23	100.0	122	2 S32574	serum amyloid prot
31	23	100.0	122	2 A30248	serum amyloid AA-3
32	23	100.0	122	2 B30248	serum amyloid AA1
33	23	100.0	122	2 C30248	serum amyloid AA2
34	23	100.0	122	2 A35660	serum amyloid-rela
35	23	100.0	122	2 J50608	serum amyloid A pr
36	23	100.0	122	2 B23843	serum amyloid prot
37	23	100.0	122	2 A23521	serum amyloid A3 p
38	23	100.0	122	2 A23843	serum amyloid prot
39	23	100.0	122	2 I49496	amyloid A - mouse
40	23	100.0	122	2 I39456	serum amyloid A2-b
41	23	100.0	122	2 I46981	serum amyloid prot
42	23	100.0	122	2 I46982	serum amyloid prot
43	23	100.0	122	4 JN0029	serum amyloid A3 p
44	23	100.0	128	1 CCRFCX	cytochrome c' - Rh
45	23	100.0	129	2 A36451	serum amyloid A1 p

ALIGNMENTS

RESULT 1

YLMNA

amyloid protein AA - American mink

C:Species: Mustela vison (American mink)

C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 05-Aug-1994

C:Accession: A03199; B03199

R:Walsh, K.; Sletten, K.; Husby, G.; Nordstoga, K.

Eur. J. Biochem. 104, 407-412, 1980

A:Title: The primary structure of amyloid fibril protein AA in endotoxin-induced amy1

A:Reference number: A03199; MUID:80156813; PMID:6767608

A:Accession: A03199

A:Molecule type: protein

A:Residues: 1-64 <MA1>

A:Accession: B03199

A:Molecule type: protein

A:Residues: 1-53 <MA2>

C:Superfamily: amyloid protein

C:Keywords: amyloid; pyroglyutamic acid

F:1-64/Product: amyloid protein AAI #status experimental <AP1>

F:1-53/Product: amyloid protein AA2 #status experimental <AP2>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 100.0%; Score 23; DB 1; Length 64;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4

DB 40 NYDA 43

RESULT 2

YLMQAR

amyloid protein AA - rhesus macaque

C:Species: Macaca mulatta (rhesus macaque)

C>Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 31-Dec-1993

C:Accession: A03198

R:Hermanson, M.A.; Kuhn, R.W.; Walsh, K.A.; Neurath, H.; Eriksen, N.; Benditt, E.P.

Biochemistry 11, 2934-2938, 1972

A:Title: Amino acid sequence of monkey amyloid protein A.

A:Reference number: A03198; MUID:7230069; PMID:4625315

A:Accession: A03198

A:Molecule type: protein

A:Residues: 1-76 <HER>

C:Superfamily: amyloid protein

C:Keywords: amyloid

Query Match 100.0%; Score 23; DB 1; Length 76;

Best Local Similarity 100.0%; Pred. No. 11e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4

Db 41 NYDA 44

RESULT 3

YLDKA

amyloid protein AA - duck (tentative sequence) (fragment)

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A03200

R:Gorevic, P.D.; Greenwald, M.; Frangione, B.; Pras, M.; Franklin, E.C.

J. Immunol. 118, 1113-1118, 1977

A:Title: The amino acid sequence of duck amyloid A (AA) protein.

A:Reference number: A03200; MUID:77142518; PMID:845435

A:Accession: A03200

A:Molecule type: protein

A:Residues: 1-80 <GOR>

A:Experimental source: Pekin breed

A:Note: although the sequence shown is homologous with other amyloid AA proteins, the appeared to be 12,000, and several additional tryptic peptides were found in low yield

C:Superfamily: amyloid protein

C:Keywords: amyloid

Query Match 100.0%; Score 23; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 45 NYDA 48

RESULT 4

I59148

apolipoprotein B - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I59148

R:Tenyson, G.E.; Sabatos, C.A.; Higuchi, K.; Meglin, N.; Brewer, H.B.

Proc. Natl. Acad. Sci. U.S.A. 86, 500-504, 1989

A:Title: Expression of apolipoprotein B mRNAs encoding higher- and lower- molecular weight

A:Reference number: I59148; MUID:89098961; PMID:2911593

A:Accession: I59148

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-80 <RES>

A:Cross-references: GB:M2049; NID:9533259; PIDN:AAA0753.1; PID:9533260

C:Genetics:

A:Gene: apob

C:Superfamily: apolipoprotein B

Query Match 100.0%; Score 23; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 74 NYDA 77

RESULT 5

I71951

serum amyloid A - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: I71951

R:Yamamoto, K.

J. Immunol. 139, 1683-1688, 1987

A:Title: Structural diversity of murine serum amyloid A genes: Evolutionary implications

A:Reference number: I55984; MUID:87309776; PMID:3624868

A:Accession: I71951

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-83 <RES>

A:Cross-references: GB:M17790; NID:9200920; PIDN:AAA0089.1; PID:9200921

C:Genetics:

A:introns: 38/2

C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 20 NYDA 23

RESULT 6

F97131

hypothetical protein CAC1877 [imported] Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: F97131

R:Moiling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: F97131

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-85 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK79841.1; PID:915024856; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1877

Query Match 100.0%; Score 23; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 4 NYDA 7

RESULT 7

YLCTA

amyloid protein AA - cat

C:Species: Felis silvestris catus (domestic cat)

C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 11-May-2000

C:Accession: J10111

R:Kluve-Beckerman, B.; Dwulet, F.E.; DiBartola, S.P.; Benson, M.D.

Comp. Biochem. Physiol. B 94, 175-183, 1989

A:Title: Primary structures of dog and cat amyloid A proteins: comparison to human AA

A:Reference number: J10110; MUID:90091422; PMID:2598632

A:Accession: J10111

A:Molecule type: protein

A:Residues: 1-90 <KLUD>

A:Note: no overlap was shown between residues 88 and 89

C:Comment: This protein is the main constituent of reactive amyloid fibrils in man and

C:Superfamily: amyloid protein

C:Keywords: amyloid

Query Match 100.0%; Score 23; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
||||
Db 40 NYDA 43

```

RESULT 8
A:Accession: A60952
amyloid protein AA - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 11-May-2000
C:Accession: A60952; A60910; A61108
R:Benson, M.D.; DiBarotola, S.P.; Dmulet, F.E.
J. Lab. Clin. Med. 113, 67-72, 1989
A:Title: A unique insertion in the primary structure of bovine amyloid AA protein.
A:Reference number: A60952; MUID:89080450; PMID:2909653
A:Accession: A60952
A:Molecule type: protein
A:Residues: 1-90 <BEN>
R:Hushekk, A.; Husby, G.; Sletten, K.; Skogen, B.; Nordstoga, K.
Scand. J. Immunol. 27, 739-743, 1988
A:Title: Characterization of bovine amyloid proteins SAA and AA.
A:Reference number: A60910; MUID:8827778; PMID:3393848
A:Accession: A60910
A:Molecule type: protein
A:Residues: 4-16 <HUS>
A:Experimental source: amyloid fibrils, kidney
A:Note: An identical fragment was sequenced from its precursor molecule serum amyloid A
R:Westermarck, P.; Johnson, K.H.; Westermarck, G.T.; Sletten, K.; Hayden, D.W.
Comp. Biochem. Physiol. B 85, 609-614, 1986
A:Title: Bovine amyloid protein AA: isolation and amino acid sequence analysis.
A:Reference number: A61108; MUID:87079535; PMID:3791962
A:Accession: A61108
A:Molecule type: protein
A:Residues: 3,'X',5-9,'X',11-13,17-20,'X',22-23,'X',25-28,'Y',30-32,'X',34-48 <MES>
C:Comment: This protein is derived from the acute phase protein serum amyloid A (SAA).
C:Comment: This protein is the main constituent of reactive amyloid fibrils in man and
C:Comment: The extracellular deposits formed by this protein are highly insoluble and re
C:Superfamily: amyloid protein
C:Keywords: acute phase; amyloid; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 40 NYDA 43

RESULT 9
S60667
phosphotransferase system phosphohistidine-containing protein - Klebsiella pneumoniae
N:Alternate names: phosphotransferase protein HPR
C:Species: Klebsiella pneumoniae
C:Date: 19-Jul-1996 #sequence_revision 31-Jan-1997 #text_change 16-Jul-1999
C:Accession: S60667
R:Merrick, M.J.; Taylor, M.
submitted to the EMBL Data Library, August 1995
A:Description: Sequence and characterisation of distal genes in the Klebsiella pneumonia
A:Reference number: S60666
A:Accession: S60667
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-90 <MER>
A:Cross-references: EMBL:250803; NID:g950054; PIDN:CAA90685.1; PID:g950056
C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotran
C:Keywords: phosphocarbonyl protein; phosphohistidine; phosphoprotein; phosphotransferase
F:9-86/Domain: phosphotransferase system phosphohistidine-containing protein homology <H
F:16/Binding site: phosphate (His) (covalent) (by phosphotransferase system enzyme 1) #s
F:48/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NYDA 4
DB 29 NYDA 32

RESULT 10
I71950
serum amyloid A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I71950
R:Yamamoto, K.
J. Immunol. 139, 1683-1688, 1987
A:Title: Structural diversity of murine serum amyloid A genes: Evolutionary implicati
A:Accession: I71950
A:Reference number: I55984; MUID:87309776; PMID:3624868
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-91 <RES>
A:Cross-references: GB:M17792; NID:g200917; PIDN:AAA40088.1; PID:g200919
C:Genetics:
A:Insertions: 46/2
C:Superfamily: amyloid protein

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 28 NYDA 31

RESULT 11
R5YM23
ribosomal protein l23 - Mycoplasma capricolum
C:Species: Mycoplasma capricolum
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-Dec-1999
C:Accession: S02833
R:Ohkubo, S.; Muto, A.; Kawachi, Y.; Yamao, F.; Osawa, S.
Mol. Gen. Genet. 210, 314-322, 1987
A:Title: The ribosomal protein gene cluster of Mycoplasma capricolum.
A:Reference number: S02830; MUID:88142549; PMID:3481422
A:Accession: S02833
A:Molecule type: DNA
A:Residues: 1-94 <OHR>
A:Cross-references: EMBL:X06414; NID:g44207; PIDN:CAA29706.1; PID:g44211
C:Genetics:
A:Gene: rpl23
A:Genetic code: SGC3
C:Superfamily: Escherichia coli ribosomal protein l23
C:Keywords: protein biosynthesis; ribosome

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 57 NYDA 60

RESULT 12
AEI789
hypothetical protein homolog lln2859 [imported] - Listeria innocua (strain C1p11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AEI789
R:Blaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
Science 294, 849-852, 2001
A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maltournam, A.;

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Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
A:Title: Comparative genomics of *Listeria* species
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1789
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC98085.1; PID:g16415394; GSPDB:GN00178
A:Experimental source: strain C1p11262
A:Genetics:
A:Gene: lln2859

Query Match 100.0%; Score 23; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 31 NYDA 34

RESULT 13
S06386
serum amyloid A protein precursor - American mink
C:Species: Mustela vison (American mink)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 05-Aug-1994
A:Accession: S06386
R:Syversen, V.; Sletten, K.; Marhaug, G.; Husby, G.; Liun, B.
Scand. J. Immunol. 26, 763-767, 1987
A:Title: The amino acid sequence of serum amyloid A (SAA) protein in mink.
A:Reference number: S06386; MUID:8809357; PMID:3423742
A:Accession: S06386
A:Molecule type: protein
A:Residues: 1-103 <SYV>
A:Note: 10-Val, 67-Val, and 71-Phe were also found
C:Superfamily: amyloid protein
C:Keywords: amyloid; pyroglyutamic acid
F:1-103/Product: amyloid protein A, serum #status experimental <MAT1>
F:1-64/Product: amyloid protein A, amyloid (long form) #status experimental <MAT2>
F:1-53/Product: amyloid protein A, amyloid (short form) #status experimental <MAT3>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 100.0%; Score 23; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 40 NYDA 43

RESULT 14
A27227
amyloid protein A - duck
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 23-Mar-1995
A:Accession: A27227; A32538
R:Ericsson, L.H.; Eriksen, N.; Walsb, K.A.; Benditt, E.P.
FEBS Lett. 218, 11-16, 1987
A:Title: Primary structure of duck amyloid protein A. The form deposited in tissues may
A:Reference number: A27227; MUID:87247238; PMID:3109944
A:Accession: A27227
A:Molecule type: protein
A:Residues: 1-106 <ERI>
A:Experimental source: Pekin breed
C:Superfamily: amyloid protein
C:Keywords: amyloid

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4

Db 45 NYDA 48

RESULT 15
AF1413
hypothetical proteins homolog lmo2711 [imported] - *Listeria monocytogenes* (strain EGD
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
A:Accession: AF1413
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fehli,
J.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madeno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1413
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00924.1; PID:g16412211; GSPDB:GN00177
A:Experimental source: strain EGD-e
A:Genetics:
A:Gene: lmo2711

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 31 NYDA 34

RESULT 16
B40085
ubiquitin carboxyl-terminal proteinase - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 11-Jan-2000
A:Accession: B40085
R:Milkinson, K.D.; Lee, K.; Deshpande, S.; Duerksen-Hughes, P.; Boss, J.M.; Pohl, J.
Science 246, 670-673, 1989
A:Title: The neuron-specific protein PCP 9.5 is a ubiquitin carboxyl-terminal hydroly
A:Reference number: A40085; MUID:90049185; PMID:2530630
A:Accession: B40085
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-108 <MIT>
C:Superfamily: human ubiquitin thiolesterase

Query Match 100.0%; Score 23; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 68 NYDA 71

RESULT 17
B82863
hypothetical protein xfa0018 [imported] - *Xylella fastidiosa* (strain 9a5c)
C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
A:Accession: B82863
R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82863

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <STM>
 C:Cross-references: GB:AF003851; NID:99112238; PIDN:AAF65587.1; GSPDB:GN00130; XFSC:XFAC
 A:Experimental source: Strain 965c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; de Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 C:Contents: annotation
 C:Genetics:
 A:Gene: XFA0018
 A:Genome: plasmid
 A:Note: plasmid pXF5.1
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 108;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NYDA 4
 1111
 Db 76 NYDA 79

RESULT 18
 B8645
 amyloid A-like protein D5A18 precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
 C:Accession: B8645
 R:Seitar, G.C.; DeBeer, M.C.; Leiliss, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P.J.
 J. Biol. Chem. 266, 3505-3510, 1991
 A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by cdn
 A:Reference number: A38645; MUID:91139635; PMID:1995613
 A:Accession: B38645
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-109 <SEB>
 A:Cross-references: GB:M59172; NID:9164061; PIDN:AAA62763.1; PID:9164062
 C:Superfamily: amyloid protein
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 109;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NYDA 4
 1111
 Db 58 NYDA 61

RESULT 19
 S26323
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
 C:Accession: S26323
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26323
 A:Molecule type: mRNA
 A:Residues: 1-110 <STG>
 A:Cross-references: EMBL:X59184; NID:952061; PIDN:CAA41894.1; PID:9134033

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:6-87/Domain: immunoglobulin homology <IMH>
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 110;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NYDA 4
 1111
 Db 93 NYDA 96

RESULT 20
 A28573
 serum amyloid A protein - horse
 N:Contains: Equus caballus (domestic horse)
 C:Species: Equus caballus (domestic horse)
 C:Date: 19-Nov-1988 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
 C:Accession: A60430; A28573
 R:Sletten, K.; Husebekk, A.; Husby, G.
 Scand. J. Immunol. 30, 117-122, 1989
 A:Title: The primary structure of equine serum amyloid A (SAA) protein.
 A:Reference number: A60430; MUID:89332320; PMID:2502829
 A:Accession: A60430
 A:Molecule type: protein
 A:Residues: 1-110 <SLB>
 A:Note: 16-Leu and 44-Gln were also found
 R:Sletten, K.; Husebekk, A.; Husby, G.
 Scand. J. Immunol. 26, 79-84, 1987
 A:Title: The amino acid sequence of an amyloid fibril protein AA isolated from the ho
 A:Reference number: A28573; MUID:87291864; PMID:3616485
 A:Accession: A28573
 A:Molecule type: protein
 A:Residues: 1-15, '17-77, 'ABZ' <SL2>
 A:Note: 44-Gln was also found; the order of residues 78-79 was uncertain
 C:Comment: Serum amyloid A protein was found to be complexed to HDL in acute phase se
 C:Superfamily: amyloid protein
 C:Keywords: amyloid
 F:1-110/Product: serum amyloid A protein #status experimental <MAT2>
 F:1-80/Product: amyloid protein A #status experimental <MAT3>
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 110;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NYDA 4
 1111
 Db 39 NYDA 42

RESULT 21
 T27515
 hypothetical protein ZC334.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27515
 R:McLay, K.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z20381
 A:Accession: T27515
 A:Status: preliminary; translated from GB/EMBL/DDBT
 A:Molecule type: DNA
 A:Residues: 1-110 <WIL>
 A:Cross-references: EMBL:Z82082; PIDN:CAB04962.1; GSPDB:GN00019; CESP:ZC334.1
 A:Experimental source: clone ZC334
 C:Genetics:
 A:Gene: CESP:ZC334.1
 A:Map position: 1
 A:Introns: 82/1
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 110;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYDA 4
 ||||
 Db 79 NYDA 82

RESULT 22
 AG1646
 hypothetical protein lin1712 [imported] - *Listeria innocua* (strain C1p11262)
 C:Species: *Listeria innocua*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1646

R:Glaser, P.; Franke, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehrl, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schuete, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1646
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-112 <GLA>
 A:Cross-references: GB:M592022; PIDN:CAC96943.1; PID:g16414199; GSPDB:GN00178
 A:Experimental source: strain C1p11262
 A:Genetics:
 A:Gene: lin1712

Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 112;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 29 NYDA 32

RESULT 23
 D38645
 amyloid A protein DSA85 precursor - dog (fragment)
 C:Species: *Canis lupus familiaris* (dog)
 C>Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
 C:Accession: D38645
 R:Sellier, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P.J.
 J. Biol. Chem. 266, 3505-3510, 1991
 A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by cDN
 A:Reference number: A38645; MUID:91139635; PMID:1995613
 A:Accession: D38645
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-116 <SEL>
 A:Cross-references: GB:M59174; NID:g164065; PIDN:AAA62765.1; PID:g164066
 C:Superfamily: amyloid protein

Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 116;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 45 NYDA 48

RESULT 24
 E38645
 amyloid A protein DSA86 precursor - dog (fragment)
 C:Species: *Canis lupus familiaris* (dog)
 C>Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
 C:Accession: E38645
 R:Sellier, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P.J.
 J. Biol. Chem. 266, 3505-3510, 1991

A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
 A:Reference number: A38645; MUID:91139635; PMID:1995613

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-116 <SEL>
 A:Cross-references: GB:M59175; NID:g164067; PIDN:AAA51457.1; PID:g164068
 C:Superfamily: amyloid protein

Query Match
 Best Local Similarity 100.0%; Score 23; DB 2; Length 116;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 45 NYDA 48

RESULT 25
 Y1DGA
 amyloid protein AA precursor (clone DSA15) - dog (fragment)
 C:Species: *Canis lupus familiaris* (dog)
 C>Date: 30-Sep-1990 #sequence_revision 12-Apr-1996 #text_change 11-May-2000
 C:Accession: A38645; J10110
 R:Sellier, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P.
 J. Biol. Chem. 266, 3505-3510, 1991
 A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
 A:Reference number: A38645; MUID:91139635; PMID:1995613
 A:Accession: A38645
 A:Molecule type: mRNA
 A:Residues: 1-119 <SEL>
 A:Cross-references: GB:M59171; NID:g164059; PIDN:AAA62762.1; PID:g164060
 R:Kluwe-Beckerman, B.; Dwyer, F.E.; DiBartola, S.P.; Benson, M.D.
 Comp. Biochem. Physiol. B 94, 175-183, 1989
 A:Title: Primary structures of dog and cat amyloid A proteins: comparison to human AA
 A:Reference number: J10110; MUID:90091422; PMID:2598632
 A:Accession: J10110
 A:Molecule type: protein
 A:Residues: 9-101 <KID>
 A:Note: 25-Trip was also found
 C:Comment: This protein is the main constituent of reactive amyloid fibrils in man an

C:Comment: The extracellular deposits formed by this protein are highly insoluble and
 C:Superfamily: amyloid protein
 C:Keywords: amyloid; pyroglyutamic acid
 F:1-8/Domain: signal sequence (fragment) #status predicted <SIG>
 F:9-101/Product: amyloid protein AA #status experimental <MAT>
 F:9/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim

Query Match
 Best Local Similarity 100.0%; Score 23; DB 1; Length 119;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 Db 48 NYDA 51

RESULT 26
 H84991
 hypothetical protein [imported] - *Buchnera* sp. (strain APS)
 C:Species: *Buchnera* sp.
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: H84991
 R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
 Nature 407, 81-86, 2000
 A:Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp
 A:Reference number: AB4930; MUID:20445173; PMID:109933077
 A:Accession: H84991
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-119 <STO>
 A:Cross-references: GB:AP000398; GSPDB:GN00144

A:Experimental source: strain APS
 C:Genetics:
 A:Gene: yhem; BU531

Query Match 100.0%; Score 23; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4
 ||||
 Db 112 NYDA 115

RESULT 27
 C38645
 amyloid A protein DSA32 precursor - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
 C:Accession: C38645
 R:Seellar, G.C.; DeBeer, M.C.; Lellis, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P.J.
 J. Biol. Chem. 266, 3505-3510, 1991
 A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by cDN
 A:Reference number: A38645; MUID:91139635; PMID:1995613
 A:Accession: C38645
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-121 <SEL>
 A:Cross-references: GB:M59173; NID:9164063; PIDN:AAA62764.1; PID:9164064
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4
 ||||
 Db 50 NYDA 53

RESULT 28
 YLH05
 serum amyloid A1 protein precursor [validated] - human
 N:Alternate names: amyloid-related serum protein SAA
 N:Contents: amyloid protein AA
 C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1992 #sequence_revision 08-Feb-1996 #text_change 08-Dec-2000
 C:Accession: A22342; S09972; S09974; S09977; S09978; S12491; S12492; S20103; A60863; A90
 3196
 R:Slupe, J.D.; Colten, H.R.; Goldberger, G.; Edge, M.D.; Tack, B.F.; Cohen, A.S.; Whitehe
 Biochemistry 24, 2931-2936, 1985
 A:Title: Human serum amyloid A (SAA): biosynthesis and postsynthetic processing of pres
 A:Reference number: A22342; MUID:85527112; PMID:3839415
 A:Contents: allele SAA1*1 (SAA1-alpha)
 A:Accession: A22342
 A:Molecule type: mRNA
 A:Residues: 1-118, 'S', 120-122 <STP>
 A:Cross-references: GB:M10906; NID:9337747; PIDN:AAA60297.1; PID:9337748
 R:Steinmasser, A.; Weiss, E.H.; Schwabe, W.; Linke, R.P.
 Biochem. J. 268, 187-193, 1990
 A:Title: Heterogeneity of human serum amyloid A protein: five different variants from or
 A:Reference number: S09972; MUID:90262544; PMID:1971508
 A:Accession: S09972
 A:Molecule type: mRNA
 A:Residues: 8-72 <STE>
 A:Cross-references: EMBL:X51443
 A:Experimental source: clone PAS4
 A>Note: allele SAA1*1 (SAA1-alpha)
 A:Accession: S09974
 A:Molecule type: mRNA
 A:Residues: 73-122 <ST2>
 A:Cross-references: EMBL:X51439; NID:936311; PIDN:CAA35804.1; PID:9825714
 A:Experimental source: clone PAS1
 A>Note: allele SAA1*1 (SAA1-alpha)

A:Accession: S09977
 A:Molecule type: mRNA
 A:Residues: 73-74, 'V', 76-77, 'N', 79-122 <ST3>
 A:Cross-references: EMBL:X51442; NID:936314; PIDN:CAA35807.1; PID:9825717
 A:Experimental source: clone PAS3-beta
 A>Note: a variant of allele SAA1-beta
 A:Accession: S09978
 A:Molecule type: mRNA
 A:Residues: 73-77, 'N', 79-122 <ST4>
 A:Cross-references: EMBL:X51441
 A:Experimental source: clone PAS3-alpha
 R:Linke, R.P.
 submitted to the EMBL Data Library, January 1990
 A:Reference number: S12491
 A:Accession: S12491
 A:Molecule type: mRNA
 A:Residues: 8-69, 'LG' <LIN>
 A:Cross-references: EMBL:X51443; NID:936315; PIDN:CAA35808.1; PID:939926
 A:Experimental source: clone PAS4
 A>Note: allele SAA1*1 (SAA1-alpha)
 A:Accession: S12492
 A:Molecule type: mRNA
 A:Residues: 73-74, 'V', 76-77, 'N', 79-122 <LI2>
 A:Cross-references: EMBL:X51441; NID:936313; PIDN:CAA35806.1; PID:9825716
 A:Experimental source: clone PAS3-alpha
 R:Betts, J.C.; Edbrooke, M.R.; Thakker, R.V.; Woo, P.
 Scand. J. Immunol. 34, 471-482, 1991
 A:Title: The human acute-phase serum amyloid A gene family: structure, evolution and
 A:Reference number: S20103; MUID:92022342; PMID:1656519
 A:Contents: allele SAA1*2b (SAA1-beta)
 A:Accession: S20103
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-69, 'A', 71-74, 'V', 76-122 <BE7>
 A:Cross-references: EMBL:X56652; NID:936307; PIDN:CAA39974.1; PID:936308
 R:Skinner, M.; Pinnette, A.; Travis, W.D.; Shwachman, H.; Cohen, A.S.
 J. Lab. Clin. Med. 112, 413-417, 1988
 A:Title: Isolation and sequence analysis of amyloid protein AA from a patient with cy
 A:Reference number: A60863; MUID:89010280; PMID:3171350
 A:Contents: allele SAA1*1 (SAA1-alpha)
 A:Accession: A60863
 A:Molecule type: protein
 A:Residues: 19-94 <SKI>
 R:Parmelee, D.C.; Titani, K.; Ericsson, L.H.; Eriksen, N.; Benditt, E.P.; Walsh, K.A.
 Biochemistry 21, 3298-3303, 1982
 A:Title: Amino acid sequence of amyloid-related apoprotein (ApoSAA-1) from human high
 A:Reference number: A90461; MUID:83000248; PMID:7115671
 A:Contents: allele SAA1*1 (SAA1-alpha)
 A:Accession: A90461
 A:Molecule type: protein
 A:Residues: 19-122 <PAR>
 A>Note: 70-Ala and 75-Val were also found
 A:Note: this protein was isolated from the high-density lipoprotein fraction of serum
 R:Sletten, K.; Marhaug, G.; Husbj, G.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 1039-1046, 1983
 A:Title: The covalent structure of amyloid-related serum protein SAA from two patient
 A:Reference number: A91711; MUID:84030495; PMID:6629328
 A:Contents: allele SAA1*1 (SAA1-alpha)
 A:Accession: A91711
 A:Molecule type: protein
 A:Residues: 19-40, 'N', 42-77, 'N', 79-92, 'N', 94-122 <SLE>
 A>Note: at least three polymorphic forms of this protein have been found in a patient
 leucine are found at position 76
 R:Prelli, F.; Pras, M.; Frangione, B.
 Biochemistry 26, 8251-8256, 1987
 A:Title: Degradation and deposition of amyloid AA fibrils are tissue specific.
 A:Reference number: A29419; MUID:88163487; PMID:3442653
 A:Contents: allele SAA1*1 (SAA1-alpha)
 A:Accession: A29419
 A:Molecule type: protein
 A:Residues: 20-100 <PRE>
 R:Westermarck, G.T.; Sletten, K.; Westermarck, P.
 Scand. J. Immunol. 30, 605-613, 1989

A:Title: Massive vascular AA-amyloidosis: a histologically and biochemically distinctive
 A:Reference number: A60431; MUID:90069444; PMID:2587936
 A:Contents: allele SAA1*1 (SAA1-alpha)
 A:Accession: A60431
 A:Molecule type: protein
 A:Residues: 19-98, 'XXXX', 103-105, 'X', 107 <WES>
 R:Beach, C.M.; de Beer, M.C.; Siipe, J.D.; Loose, L.D.; de Beer, F.C.
 Biochem. J. 282, 615-620, 1992
 A:Title: Human serum amyloid A protein. Complete amino acid sequence of a new variant.
 A:Reference number: S21260; MUID:92189607; PMID:1546977
 A:Contents: allele SAA1*2a (SAA1-beta)
 A:Accession: S21261
 A:Molecule type: protein
 A:Residues: 19-69, 'A', 71-74, 'V', 76-89, 'D', 91-122 <BEA>
 A:Accession: S21260
 A:Molecule type: protein
 A:Residues: 20-69, 'A', 71-74, 'V', 76-89, 'D', 91-122 <BE2>
 R:Baba, S.; Takahashi, T.; Kasama, T.; Fujie, M.; Shitrasawa, H.
 Arch. Biochem. Biophys. 303, 361-366, 1993
 A:Title: A novel polymorphism of human serum amyloid A protein, SAA1gamma, is characteri
 A:Reference number: S33864; MUID:93290347; PMID:8512321
 A:Contents: allele SAA1-gamma
 A:Accession: S33864
 A:Molecule type: protein
 A:Residues: 19-69, 'A', 71-122 <BAB>
 R:Baba, S.; Takahashi, T.; Kasama, T.; Shitrasawa, H.
 Biochem. Biophys. Acta 1180, 195-200, 1992
 A:Title: Identification of two novel amyloid A protein subtypes coexisting in an individ
 A:Reference number: A56867; MUID:93099171; PMID:1463770
 A:Contents: allele SAA1-gamma (allele 52,57-Ala)
 A:Accession: A56867
 A:Molecule type: protein
 A:Residues: 65-69, 'A', 71-80 <BA2>
 A:Experimental source: amyloid fibrils, thyroid gland of rheumatoid arthritis patient
 A:Note: sequence extracted from NCBI backbone (NCBI:121042)
 R:Moynier, K.; Sletten, K.; Husby, G.; Natvig, J.B.
 Scand. J. Immunol. 11, 549-554, 1980
 A:Title: An unusually large (83 amino acid residues) amyloid fibril protein AA from a pa
 A:Reference number: A94234; MUID:80213686; PMID:6155694
 A:Contents: B01
 A:Accession: A94234
 A:Molecule type: protein
 A:Residues: 19-40, 'N', 42-83, 'E', 85-92, 'N', 94-95, 'SEATVK' <MOY>
 A:Note: 70-Ala and 71-Arg were also found
 A:Note: this protein is from a patient with Waldenstrom's macroglobulinemia
 R:Sletten, K.; Husby, G.
 Eur. J. Biochem. 41, 117-125, 1974
 A:Title: The complete amino-acid sequence of non-immunoglobulin amyloid fibril protein A
 A:Reference number: A91215; MUID:74120351; PMID:4816450
 A:Contents: Th
 A:Accession: A91215
 A:Molecule type: protein
 A:Residues: 19-40, 'N', 42-92, 'N', 94 <SL3>
 A:Note: this protein is from a patient with juvenile rheumatoid arthritis
 R:Sletten, K.; Husby, G.; Natvig, J.B.
 Biochem. Biophys. Res. Commun. 69, 19-25, 1976
 A:Title: The complete amino acid sequence of an amyloid fibril protein AA of unusual siz
 A:Reference number: A90195; MUID:76160745; PMID:1259755
 A:Contents: J1
 A:Accession: A90195
 A:Molecule type: protein
 A:Residues: 19-40, 'N', 42-77, 'N', 79-82 <SL2>
 A:Note: 19-Arg is missing from some of the molecules
 A:Note: this protein is from a patient with ankylosing spondylitis
 R:Gorevic, P.D.; Prelli, F.C.; Wright, J.; Pras, M.; Frangione, B.
 J. Clin. Invest. 83, 836-843, 1989
 A:Title: Systemic senile amyloidosis. Identification of a new prealbumin (transferrin)
 A:Reference number: A30323; MUID:89155805; PMID:2646319
 A:Accession: B30323
 A:Molecule type: protein
 A:Residues: 19-29 <GOR>
 R:Ohlar, C.M.; Burgess, C.J.; Sharp, P.M.; Whitehead, A.S.

Genomics 19, 228-235, 1994
 A:Title: Evolution of the serum amyloid A (SAA) protein superfamily.
 A:Reference number: A38975; MUID:94245191; PMID:8188253
 A:Contents: annotation
 R:Krive-Beckerman, B.; Dwyer, F.E.; Benson, M.D.
 J. Clin. Invest. 82, 1670-1675, 1988
 A:Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins in
 A:Reference number: 139454; MUID:89034862; PMID:3183061
 A:Accession: 139454
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122 <RES>
 A:Cross-references: GB:M23698; NID:g758678; PIDN:AAA64799.1; PID:g758679
 C:Genetics:
 A:Gene: GDB:SAA1; SAA
 A:Cross-references: GDB:120364; OMIM:104750
 A:Map position: 11p15.1-11p15.1
 A:Introns: 31/71; 77/2
 C:Superfamily: amyloid protein
 C:Keywords: acute phase; amyloid; HDL; polymorphism
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-122/Product: (or 20-122) serum amyloid A1 protein #status experimental <APA>
 F:19-94/Product: (or 20-94) amyloid protein AA #status experimental <AP3>
 Query Match 100.0%; Score 23; DB 1; Length 122;
 Best local similarity 100.0%; Pred. No. 1; Be+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYDA 4
 Db 59 NYDA 62
 RESULT 29
 YLHUA
 serum amyloid A2 protein precursor [validated] - human
 N:Alternate names: amyloid IV; amyloid protein AA (FMP); amyloid-related serum protei
 C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence revision 08-Feb-1996 #text change 08-Dec-2000
 C:Accession: A27902; S20104; S09975; S09976; S09973; B38974; A28445; A92763; A92112;
 R:Krive-Beckerman, B.; Jong, G.L.; Benson, M.D.
 Biochem. Genet. 24, 795-803, 1986
 A:Title: DNA sequence evidence for polymorphic forms of human serum amyloid A (SAA).
 A:Reference number: A27902; MUID:87099785; PMID:3800865
 A:Contents: allele SAA2*1 (SAA2-alpha)
 A:Accession: A27902
 A:Molecule type: mRNA
 A:Residues: 1-122 <KIU>
 A:Cross-references: GB:M26152; NID:g1160968; PIDN:AAA85338.1; PID:g1160969
 R:Bets, J.C.; Edbrooke, M.R.; Thakker, R.V.; Woo, P.
 Scand. J. Immunol. 34, 471-482, 1991
 A:Title: The human acute-phase serum amyloid A gene family: structure, evolution and
 A:Reference number: S20103; MUID:9202342; PMID:1656519
 A:Contents: allele SAA2*1 (SAA2-alpha)
 A:Accession: S20104
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 32-122 <BET>
 A:Cross-references: EMBL:X56653; NID:g36309; PIDN:CAA39975.1; PID:g36310
 R:Steinkasserer, A.; Weiss, E.H.; Schwaedle, W.; Linke, R.P.
 Biochem. J. 268, 187-193, 1990
 A:Title: Heterogeneity of human serum amyloid A protein: five different variants from
 A:Reference number: S09972; MUID:90262544; PMID:1971508
 A:Accession: S09975
 A:Molecule type: mRNA
 A:Residues: 1-55 <STE>
 A:Cross-references: EMBL:X51444; NID:g36316; PIDN:CAA35809.1; PID:g36317
 A:Experimental source: clone PAS6
 A:Note: allele SAA2*1 (SAA2-alpha)
 A:Accession: S09976
 A:Molecule type: mRNA
 A:Residues: 4-122 <ST2>
 A:Cross-references: EMBL:X51445; NID:g36320; PIDN:CAA35810.1; PID:g36321

A:Experimental source: clone PAS8
 A:Note: allele SAA2*1 (SAA2-alpha)
 A:Accession: S05973
 A:Molecule type: mRNA
 A:Residues: 73-88, 'R', 90-122 <ST3>
 A:Cross-references: EMBL:Y51440; NID:936312; PIDN:CAA5805.1; PID:g825715
 A:Experimental source: clone PAS2
 A:Note: allele SAA2*2 (SAA2-beta)
 R:Steele, D.M.; Sellar, G.C.; Uhlar, C.M.; Simon, S.; DeBeer, F.C.; Whitehead, A.S.
 Genomics 16, 447-454, 1993
 A:Title: A constitutively expressed serum amyloid A protein gene (SAA4) is closely linked
 A:Reference number: A38974; MUID:93300520; PMID:7686132
 A:Contents: allele SAA2*2 (SAA2-beta)
 A:Accession: B38974
 A:Molecule type: DNA
 A:Residues: 1-88, 'R', 90-122 <ST4>
 A:Cross-references: GB:L05921
 R:Woo, P.; Sipe, J.; Dinarello, C.A.; Colten, H.R.
 J. Biol. Chem. 262, 15790-15795, 1987
 A:Title: Structure of a human serum amyloid A gene and modulation of its expression in t
 A:Reference number: A28445; MUID:88058926; PMID:2850635
 A:Contents: allele SAA2*2 (SAA2-beta)
 A:Accession: A28445
 A:Molecule type: DNA
 A:Residues: 1-14, 'G', 16-88, 'R', 90-122 <WOO>
 A:Cross-references: GB:J03474; NID:9337742; PIDN:AB59539.1; PID:g337743
 R:Levin, M.; Franklin, E.C.; Frangione, B.; Pras, M.
 J. Clin. Invest. 51, 2773-2776, 1972
 A:Title: The amino acid sequence of a major nonimmunoglobulin component of some amyloid
 A:Reference number: A92763; MUID:72268653; PMID:5056669
 A:Contents: allele SAA2*2 (SAA2-beta)
 A:Accession: A92763
 A:Molecule type: protein
 A:Residues: 19-70, 'R', 72-88, 'R', 90-94 <LEV>
 A:Note: this protein is from a patient with familial Mediterranean fever
 A:Note: the sequence of residues 19-72 of amyloid protein AA from a patient with tubercu
 R:Elm, D.; Kimura, S.; Terry, W.D.; Magnotta, J.; Glenner, G.G.
 J. Biol. Chem. 247, 5653-5655, 1972
 A:Title: Amino acid sequence of an amyloid fibril protein of unknown origin.
 A:Reference number: A92112; MUID:7226694; PMID:5055786
 A:Accession: A92112
 A:Molecule type: protein
 A:Residues: 19-63 <EIN>
 A:Note: this amyloid IV was isolated from a patient with rheumatoid arthritis
 R:Benditt, E.P.; Eriksen, N.; Hermodson, M.A.; Ericsson, L.H.
 FEBS Lett. 19, 169-173, 1971
 A:Title: The major proteins of human and monkey amyloid substance: common properties and
 A:Reference number: A91345
 A:Accession: A91345
 A:Molecule type: protein
 A:Residues: 19-42 <BEN>
 A:Note: the amino-terminal tripeptide is sometimes missing
 A:Note: this protein is from a patient with generalized amyloidosis associated with tube
 R:Baba, S.; Takahashi, T.; Kaama, T.; Shirasawa, H.
 Biochim. Biophys. Acta 1180, 195-200, 1992
 A:Title: Identification of two novel amyloid A protein subtypes coexisting in an individu
 A:Reference number: A56867; MUID:93099171; PMID:1463770
 A:Contents: allele SAA2*1 (SAA2-alpha)
 A:Accession: B56867
 A:Molecule type: protein
 A:Residues: 65-80 <BAB>
 A:Experimental source: amyloid fibrils, thyroid gland of rheumatoid arthritis patient
 A:Note: sequence extracted from NCBI Backbone (NCBI:P121046)
 R:Klive-Beckerman, B.; Dvulet, F.E.; Benson, M.D.
 J. Clin. Invest. 82, 1670-1675, 1988
 A:Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins in or
 A:Reference number: I39454; MUID:89034862; PMID:3183061
 A:Accession: I39455
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122 <RES>
 A:Cross-references: GB:M23699; NID:g758680; PIDN:AAA64800.1; PID:g758681
 C:Genetics:

A:Gene: GDB:SAA2
 A:Cross-references: GDB:132592; OMIM:104751
 A:Map position: 11p15.1-11p15.1
 A:introns: 31/1; 77/2
 C:Superfamily: amyloid protein
 C:Keywords: acute phase; amyloid; polymorphism
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-94/Product: serum amyloid A2 protein #status experimental <MAT>
 Query Match 100.0%; Score 23; DB 1; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NYDA 4
 Db 59 NYDA 62
 RESULT 30
 S32574
 serum amyloid protein SAA - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S32574
 R:Mitchell, T.I.; Coon, C.I.; Brinckerhoff, C.E.
 J. Clin. Invest. 87, 1177-1185, 1991
 A:Title: Serum amyloid A (SAA3) produced by rabbit synovial fibroblasts treated with
 A:Reference number: S32574; MUID:91185595; PMID:1849144
 A:Accession: S32574
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-122 <MIT>
 A:Cross-references: EMBL:M64696; NID:g165698; PIDN:AAA31464.1; PID:g165699
 C:Superfamily: amyloid protein
 Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NYDA 4
 Db 59 NYDA 62

RESULT 31
 A30248
 serum amyloid AA-3 - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 30-Sep-1993
 C:Accession: A30248
 R:Webb, C.F.; Tucker, P.W.; Dowton, S.B.
 Biochemistry 28, 4785-4790, 1989
 A:Title: Expression and sequence analyses of serum amyloid A in the Syrian hamster.
 A:Reference number: A30248; MUID:99352552; PMID:2765510
 A:Accession: A30248
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-122 <WEB>
 C:Superfamily: amyloid protein
 Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NYDA 4
 Db 59 NYDA 62
 RESULT 32
 B30248
 serum amyloid AAI - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)

C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 30-Sep-1993
 C:Accession: B30248
 R:Webb, C.F.; Tucker, P.W.; Dorton, S.B.
 Biochemistry 28, 4785-4790, 1989
 A:Title: Expression and sequence analyses of serum amyloid A in the Syrian hamster.
 A:Reference number: A30248; MUID:89352552; PMID:2765510
 A:Accession: B30248
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-122 <WEB>
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 Db 59 NYDA 62

RESULT 33
 C30248
 serum amyloid AA2 - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 17-Feb-1994
 C:Accession: C30248
 R:Webb, C.F.; Tucker, P.W.; Dorton, S.B.
 Biochemistry 28, 4785-4790, 1989
 A:Title: Expression and sequence analyses of serum amyloid A in the Syrian hamster.
 A:Reference number: A30248; MUID:89352552; PMID:2765510
 A:Accession: C30248
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-122 <WEB>
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 Db 59 NYDA 62

RESULT 34
 A35660
 serum amyloid-related protein SAA3 - hamster
 C:Species: Cricetinae gen. sp. (hamster)
 C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 20-Aug-1999
 C:Accession: A35660
 R:Gervais, C.; Suh, M.
 Mol. Cell. Biol. 10, 4412-4414, 1990
 A:Title: Serum amyloid A protein-related mRNA expression in herpes simplex virus type 2
 A:Reference number: A35660; MUID:90318412; PMID:2164641
 A:Accession: A35660
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-122 <GER>
 A:Cross-references: GB:M3431; NID:9191440; PIDN:AAA37098.1; PID:9305362
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 Db 59 NYDA 62

RESULT 35

JS0608
 serum amyloid A protein precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
 C:Accession: JS0608; JN0076; S13704; S13705; S14435; A54319
 R:Ray, B.K.; Ray, A.
 Biochem. Biophys. Res. Commun. 180, 1258-1264, 1991
 A:Title: Rabbit serum amyloid A gene: cloning, characterization and sequence analysis
 A:Reference number: JS0608; MUID:92062152; PMID:1953777
 A:Accession: JS0608
 A:Molecule type: DNA
 A:Residues: 1-122 <RAY>
 R:Ray, B.K.; Ray, A.
 Biochem. Biophys. Res. Commun. 178, 68-72, 1991
 A:Title: Complementary DNA cloning and nucleotide sequence of rabbit serum amyloid A
 A:Reference number: JN0076; MUID:9198985; PMID:1712590
 A:Accession: JN0076
 A:Molecule type: mRNA
 A:Residues: 1-122 <RA2>
 R:Ratam, F.; Alam, J.; Smith, A.; Morgan, W.T.
 Nucleic Acids Res. 18, 7447, 1990
 A:Title: Molecular cloning, nucleotide sequence heterozygosity and regulation of rabb
 A:Reference number: S13704; MUID:91081342; PMID:2259638
 A:Accession: S13704
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 54-122 <TAT>
 A:Cross-references: EMBL:X16427; NID:91449; PIDN:CAA34450.1; PID:91450
 A:Accession: S13705
 A:Molecule type: mRNA
 A:Residues: 1-39, 'S', 'A', '1-96, 'G', '98-122 <TAT>
 A:Cross-references: EMBL:X16428
 A>Note: the authors translated the codon GGC for residue 97 as Ala
 R:Ratam, F.M.
 submitted to the EMBL Data Library, September 1989
 A:Reference number: S14435
 A:Accession: S14435
 A:Molecule type: mRNA
 A:Residues: 1-39, 'S', 'A', '1-95, 'A', '97-122 <TAT>
 A:Cross-references: EMBL:X16428; NID:91451; PIDN:CAA34451.1; PID:91452
 R:Ratam, F.M.; Dwyer, F.E.; Benson, M.D.; Kluge-Beckerman, B.; Kushner, I.
 U. Lab. Clin. Med. 118, 570-575, 1991
 A:Title: The primary structure of serum amyloid A protein in the rabbit: comparison w
 A:Reference number: A54319; MUID:92078744; PMID:1744506
 A:Accession: A54319
 A:Molecule type: protein
 A:Residues: 'E', '20-81, 'A', '83-122 <LIE>
 A:Experimental source: acute-phase serum
 A>Note: sequence extracted from NCBI backbone (NCBIP:68876)
 C:Genetics:
 A:Introns: 30/2; 77/2
 C:Superfamily: amyloid protein
 C:Keywords: amyloid
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-122/Product: serum amyloid A protein #status predicted <NAT>

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 Db 59 NYDA 62

RESULT 36
 B23843
 serum amyloid protein SAA2 precursor - mouse
 N:Contains: amyloid protein SAA2
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Aug-1999
 C:Accession: B23843; B2675; A60864; S21287; S22427; I55984
 R:Lowell, C.A.; Potter, D.A.; Stearman, R.S.; Morrow, J.F.

J. Biol. Chem. 261, 8442-8452, 1986
 A:Title: Structure of the murine serum amyloid A gene family. Gene conversion.
 A:Reference number: A23843; MUID:86250747; PMID:3013853
 A:Accession: B23843
 A:Molecule type: DNA
 A:Residues: 1-122 <LOW>
 A:Cross-references: GB:M13522; NID:g200910; PIDN:AAA40086.1; PID:g200911
 R:Yamamoto, K.I.; Migita, S.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2915-2919, 1985
 A:Title: Complete primary structures of two major murine serum amyloid A proteins deduced
 A:Reference number: A94041; MUID:85190607; PMID:3857624
 A:Accession: B2675
 A:Molecule type: mRNA
 A:Residues: 1-122 <YAM>
 A:Cross-references: GB:M11130; NID:g200908; PIDN:AAA40085.1; PID:g200909
 R:DWulet, F.E.; Benson, M.D.
 J. Lab. Clin. Med. 110, 322-329, 1987
 A:Title: Primary structure of amyloid fibril protein AA in azocasein-induced amyloidosis
 A:Reference number: A60864; MUID:87282056; PMID:3611954
 A:Accession: A60864
 A:Molecule type: protein
 A:Residues: 20-92 <DMU>
 A:Experimental source: strain CBA/J
 R:Eriksen, N.; Ericsson, L.H.; Pearlsall, N.; Lagunoff, D.; Benditt, E.P.
 Proc. Natl. Acad. Sci. U.S.A. 73, 964-967, 1976
 A:Title: Mouse amyloid protein AA: homology with nonimmunoglobulin protein of human and
 A:Reference number: A12268; MUID:76152375; PMID:815910
 A:Accession: A12268
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 20-47 <ERI>
 R:de Beer, M.C.; de Beer, F.C.; Beach, C.M.; Carreiras, I.; Sipe, J.D.
 Biochem. J. 283, 673-678, 1992
 A:Title: Mouse serum amyloid A protein. Complete amino acid sequence and mRNA analysis
 A:Reference number: S21287; MUID:92272662; PMID:1590757
 A:Accession: S21287
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 20-119, 'D', 121-122 <BE2>
 R:Yamamoto, K.
 J. Immunol. 139, 1683-1688, 1987
 A:Title: Structural diversity of murine serum amyloid A genes: Evolutionary implications
 A:Reference number: I55984; MUID:87309776; PMID:3624868
 A:Accession: I55984
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 32-122 <RES>
 A:Cross-references: GB:M1791; NID:g200913; PIDN:AAA40087.1; PID:g200915
 C:Genetics: SAA2
 A:Gene: SAA2
 A:Map position: 7
 A:Introns: 31/1; 77/2
 C:Superfamily: amyloid protein
 C:Keywords: amyloid
 F:1-19/Domains: signal sequence #status predicted <SIG>
 F:20-122/Product: serum amyloid protein SAA2 #status predicted <MAT1>
 F:20-92/Product: amyloid A protein SAA2 #status experimental <MAT2>

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 DB 59 NYDA 62

RESULT 37
 A23521

serum amyloid A3 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Aug-1999
 C:Accession: A23521; B23521; C23843; I49495
 R:Stearman, R.S.; Lowell, C.A.; Peltzman, C.G.; Morrow, J.F.
 Nucleic Acids Res. 14, 797-809, 1986
 A:Title: The sequence and structure of a new serum amyloid A gene.
 A:Reference number: A23521; MUID:86120372; PMID:3003697
 A:Accession: A23521
 A:Molecule type: DNA
 A:Residues: 1-30 <ST1>
 A:Accession: B23521
 A:Molecule type: mRNA
 A:Residues: 27-122 <ST2>
 A:Cross-references: GB:X03479; NID:g54035; PIDN:CAA27199.1; PID:g817998
 R:Lowell, C.A.; Potter, D.A.; Stearman, R.S.; Morrow, J.F.
 J. Biol. Chem. 261, 8442-8452, 1986
 A:Title: Structure of the murine serum amyloid A gene family. Gene conversion.
 A:Reference number: A23843; MUID:86250747; PMID:3013853
 A:Accession: C23843
 A:Molecule type: DNA
 A:Residues: 1-122 <LOW>
 R:Stearman, R.S.; Lowell, C.A.; Pearson, W.R.; Morrow, J.F.
 Ann. N. Y. Acad. Sci. 389, 106-115, 1982
 A:Title: Regulation of synthesis of amyloid A-related protein.
 A:Reference number: I49495; MUID:82229376; PMID:6953913
 A:Accession: I49495
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 27-64 <RES>
 A:Cross-references: GB:M25467; NID:g191929; PIDN:AAA37231.1; PID:g191930
 C:Genetics: SAA1
 A:Introns: 31/1; 77/2
 C:Superfamily: amyloid protein
 C:Keywords: acute phase; amyloid
 F:19-122/Product: serum amyloid-related protein SAA3 #status predicted <MAT>

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 DB 59 NYDA 62

RESULT 38
 A23843

serum amyloid protein SAA1 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Aug-1999
 C:Accession: A23843; A22675
 R:Lowell, C.A.; Potter, D.A.; Stearman, R.S.; Morrow, J.F.
 J. Biol. Chem. 261, 8442-8452, 1986
 A:Title: Structure of the murine serum amyloid A gene family. Gene conversion.
 A:Reference number: A23843; MUID:86250747; PMID:3013853
 A:Accession: A23843
 A:Molecule type: DNA
 A:Residues: 1-122 <LOW>
 A:Cross-references: GB:M13521; NID:g200905; PIDN:AAA40084.1; PID:g200906
 R:Yamamoto, K.I.; Migita, S.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2915-2919, 1985
 A:Title: Complete primary structures of two major murine serum amyloid A proteins ded
 A:Reference number: A94041; MUID:85190607; PMID:3857624
 A:Accession: A22675
 A:Molecule type: mRNA
 A:Residues: 9-122 <YAM>
 A:Cross-references: GB:M11131; NID:g200903; PIDN:AAA40083.1; PID:g200904
 C:Genetics: SAA1
 A:Gene: SAA1
 A:Map position: 7
 A:Introns: 31/1; 77/2
 C:Superfamily: amyloid protein

C:Keywords: amyloid
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-122/Product: serum amyloid protein SAA1 #status predicted <MAT>

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 DB 59 NYDA 62

RESULT 39
 I49496
 amyloid A - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
 C:Accession: I49496
 R:de Beer, M.C.; de Beer, F.C.; McCubbin, W.D.; Kay, C.M.; Kindy, M.S.
 J. Biol. Chem. 268, 20606-20612, 1993
 A:Title: Structural prerequisites for serum amyloid A fibril formation.
 A:Reference number: A48020; MUID:93388642; PMID:8376413
 A:Accession: I49496
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122 <RES>
 A:Cross-references: GB:I22190; NID:g404752; PIDN:AAA19818.1; PID:g404753
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 DB 59 NYDA 62

RESULT 40
 I39456
 serum amyloid A2-beta - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 20-Aug-1999
 C:Accession: I39456
 R:Kliver-Beckerman, B.; Dwulet, F.E.; Benson, M.D.
 J. Clin. Invest. 82, 1670-1675, 1988
 A:Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins in or
 A:Reference number: I39454; MUID:89034862; PMID:3183061
 A:Accession: I39456
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122 <RES>
 A:Cross-references: GB:M2700; NID:g758682; PIDN:AAA64801.1; PID:g758683
 C:Genetics:
 A:Gene: GDB:SAA2
 A:Cross-references: GDB:I32592; OMIM:104751
 A:Map position: 11p15.1-11p15.1
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 DB 59 NYDA 62

RESULT 41
 I46981
 serum amyloid protein A - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
 C:Accession: I46981
 R:Rygg, M.; Marnaug, G.; Husby, G.; Dowton, S.B.
 Scand. J. Immunol. 34, 727-734, 1991

A:Title: Rabbit serum amyloid protein A: expression and primary structure deduced fro
 A:Reference number: I46981; MUID:92086827; PMID:1721234
 A:Accession: I46981

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122 <RYG>
 A:Cross-references: GB:S71722; NID:g240621; PIDN:AAB20616.1; PID:g240622
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 DB 59 NYDA 62

RESULT 42
 I46982
 serum amyloid protein A - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
 C:Accession: I46982
 R:Rygg, M.; Marnaug, G.; Husby, G.; Dowton, S.B.
 Scand. J. Immunol. 34, 727-734, 1991
 A:Title: Rabbit serum amyloid protein A: expression and primary structure deduced fro
 A:Reference number: I46981; MUID:92086827; PMID:1721234
 A:Accession: I46982
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-122 <RYG>
 A:Cross-references: GB:S71725; NID:g240623; PIDN:AAB20617.1; PID:g240624
 C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
 ||||
 DB 59 NYDA 62

RESULT 43
 JN0029
 serum amyloid A3 pseudogene - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 17-May-1996 #text_change 20-Apr-2000
 C:Accession: JN0029
 R:Sack Jr., G.H.; Talbot Jr., C.C.
 Gene 84, 509-515, 1989
 A:Title: The human serum amyloid A (SAA)-encoding gene GSA1: nucleotide sequence and
 A:Reference number: JN0029
 A:Accession: JN0029
 A:Status: conceptual translation of pseudogene
 A:Molecule type: DNA
 A:Residues: 1-122 <SAC>
 A:Cross-references: EMBL:X13895; NID:g36305; PIDN:CAA32096.1; PID:g36306
 R:Stiel, D.M.; Sellar, G.C.; Uhlar, C.M.; Simon, S.; DeBeer, F.C.; Whitehead, A.S.
 Genomics 16, 447-454, 1993
 A:Title: A constitutively expressed serum amyloid A protein gene (SAA4) is closely li
 A:Reference number: A38974; MUID:93300520; PMID:7686132
 A:Contents: annotation
 A:Note: references cited confirm a frameshift error between codons 30 and 32 that lea
 C:Genetics:
 A:Gene: GDB:SAA3; GSA1
 A:Cross-references: GDB:I32593
 A:Map position: 11p15.1-p14

A:Introns: 31/1: 77/2
C:Keywords: pseudogene

Query Match 100.0%; Score 23; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 59 NYDA 62

RESULT 44

CCRCX

cytochrome c' - Rhodopseudomonas sp.

C:Species: Rhodopseudomonas sp.

C>Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 03-Mar-2000

C:Accession: A00139

R:Ambler, R.P.; Bartsch, R.G.; Daniel, M.; Kamen, M.D.; McLellan, L.; Meyer, T.E.; Van E

Proc. Natl. Acad. Sci. U.S.A. 78, 6854-6857, 1981

A>Title: Amino acid sequences of bacterial cytochromes c' and c-556.

A:Reference number: A93899; MUID:82082545; PMID:6273892

A:Accession: A00139

A:Molecule type: protein

A:Residues: 1-128 <AMB>

A:Experimental source: strain T312

C:Superfamily: cytochrome c'

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein

F;117,120/Binding site: heme (Cys) (covalent) #status predicted

F;121/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 100.0%; Score 23; DB 1; Length 128;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 29 NYDA 32

RESULT 45

A36451

serum amyloid A1 precursor - American mink

C:Species: Mustela vison (American mink)

C>Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 20-Aug-1999

C:Accession: A36451

R:Marhaug, G.; Husby, G.; Dowton, S.B.

J. Biol. Chem. 265, 10049-10054, 1990

A>Title: Mink serum amyloid A protein. Expression and primary structure based on cDNA se

A:Reference number: A36451; MUID:90277614; PMID:2351648

A:Accession: A36451

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-129 <MAR>

A:Cross-references: GB:M4953; GB:J05445; NID:g164265; P1DN:AAA30968.1; PID:g164266

C:Superfamily: amyloid protein

Query Match 100.0%; Score 23; DB 2; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
|||
Db 58 NYDA 61

Search completed: February 6, 2003, 11:23:10
Job time : 12.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 5.33333 Seconds
(without alignments)
31.107 Million cell updates/sec

Title: PAT943-5
Perfect score: 23
Sequence: 1 nyda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 223

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	23	100.0	76	1 SAA_MACMU	P02738 macaca mula
2	23	100.0	90	1 PTSO_KLEPN	P51185 klebsiella
3	23	100.0	90	1 SAA_FELCA	P19707 felis silve
4	23	100.0	94	1 RL23_MYCCA	P10140 mycoplasma
5	23	100.0	102	1 SAA5_MESAU	P81491 mesocricetu
6	23	100.0	110	1 SAA_HORSE	P19857 equus cabal
7	23	100.0	112	1 SAA_BOVIN	P35341 bos taurus
8	23	100.0	112	1 SAA_SHEEP	P42819 ovis aries
9	23	100.0	119	1 Y531_BUCAL	P57597 bucheira ap
10	23	100.0	122	1 SAA1_MESAU	P20726 mesocricetu
11	23	100.0	122	1 SAA1_MOUSE	P50366 mus musculu
12	23	100.0	122	1 SAA1_RABIT	P53614 oryctolagus
13	23	100.0	122	1 SAA2_MESAU	P20727 mesocricetu
14	23	100.0	122	1 SAA2_MOUSE	P05367 mus musculu
15	23	100.0	122	1 SAA2_RABIT	P22000 oryctolagus
16	23	100.0	122	1 SAA3_HUMAN	P22614 homo sapien
17	23	100.0	122	1 SAA3_MESAU	P19453 mesocricetu
18	23	100.0	122	1 SAA3_MOUSE	P49198 mus musculu
19	23	100.0	122	1 SAA3_RABIT	P35543 oryctolagus
20	23	100.0	122	1 SAA_HUMAN	P02735 homo sapien
21	23	100.0	127	1 SAA_ANAPL	P02740 anas platyr
22	23	100.0	127	1 SAA_MACEU	P53613 macropus eu
23	23	100.0	128	1 CYCP_RHOSP	P00146 rhodopsu
24	23	100.0	129	1 SAA1_MOUSE	P18575 mustela vis
25	23	100.0	129	1 SAA2_MOUSE	P02739 mustela vis
26	23	100.0	129	1 SAA_CANFA	P19708 canis fami
27	23	100.0	130	1 SAA4_HUMAN	P35542 homo sapien
28	23	100.0	142	1 COAC_HUMAN	P01410 homo sapien
29	23	100.0	142	1 COAC_MOUSE	P09916 mus musculu
30	23	100.0	144	1 RIB1_PHOLE	P01994 photobacter
31	23	100.0	154	1 RIBB_STRAAM	P03118 staphylococ
32	23	100.0	159	1 FME5_ECOLI	P13719 escherichia
33	23	100.0	160	1 UBCG_SCHPO	O9p611 schizosacch

ALIGNMENTS

RESULT 1	ID	SAA_MACMU	STANDARD:	PRT:	76 AA.
AC	P02738;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Amyloid protein A (Amyloid fibril protein AA).				
OS	Macaca mulatta (Rhesus macaque).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;				
OC	Cercopitheciinae; Macaca.				
OX	NCBI_Taxid=9544;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=72230069; PubMed=4625315.				
RA	Hernodson W.A., Kunz R.W., Walsh K.A., Neurath H., Eriksen N.,				
RA	Benditt E.P.;				
RT	*Amino acid sequence of monkey amyloid protein A.*;				
RL	Biochemistry 11:2934-2938(1972).				
CC	- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL				
CC	COMPLEX.				
CC	- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.				
CC	- INDUCTION: UPON CYTOKINE STIMULATION.				
CC	- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE				
CC	EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.				
CC	THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;				
CC	THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.				
CC	- SIMILARITY: BELONGS TO THE SAA FAMILY.				
DR	PIR; A03198; YLMQAR.				
DR	InterPro: IPR000096; Serum_amyloid_A.				
DR	Pfam: PF00277; SAA_proteins; 1.				
DR	PRINTS: PR00306; SERUMAMYLOID.				
DR	ProDom: PD002112; Serum_amyloid_A; 1.				
DR	SMART; SM00197; SAA; 1.				
DR	PROSITE; PS00992; SAA; 1.				
KW	Acute phase; Plasma; HDL; Amyloid.				
SQ	SEQUENCE 76 AA; 8620 MW; A2E3905B32EDDED4 CRC64;				
Query Match 100.0%; Score 23; DB 1; Length 76;					
Best Local Similarity 100.0%; Pred. NO. 36;					
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1 NYDA 4				
DB	41 NYDA 44				
RESULT 2					
ID	PTSO_KLEPN	STANDARD:	PRT:	90 AA.	
AC	P51185;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Phosphocarrier protein Npr (Nitrogen related Hpr).				

34	23	100.0	163	1 TPX_STRPA	P31307 streptococc
35	23	100.0	165	1 PHA2_SYNPY	P27646 synechococc
36	23	100.0	165	1 TPX_PASMU	P57880 pasteurella
37	23	100.0	197	1 WRBA_ECO57	O8x4b4 escherichia
38	23	100.0	202	1 YCP2_PSEA9	P29300 pseudanabae
39	23	100.0	205	1 Y363_LISMO	P58495 listeria mo
40	23	100.0	209	1 Y382_LISIN	O92es6 listeria in
41	23	100.0	230	1 UBL3_HUMAN	P15374 homo sapien
42	23	100.0	230	1 UBL3_MOUSE	O91kbl1 mus musculu
43	23	100.0	233	1 HEX8_ADE40	P11821 human adeno
44	23	100.0	233	1 HEX8_ADE41	P11822 human adeno
45	23	100.0	233	1 UBL4_MOUSE	P58321 mus musculu

```

GN      PTSO OR NPR.
OS      Klebsiella pneumoniae.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Klebsiella.
OX      NCBI_TaxID=573;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      STRAIN=M5a1;
RA      Merrick M.J., Taylor M.;
RL      Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: SEEMS TO HAVE A ROLE IN LINKING CARBON AND NITROGEN
CC      ASSIMILATION. PROBABLY ACT IN A REGULATORY CAPACITY AND COULD
CC      CONTROL THE STATE OF PHOSPHORYLATION OF IIA-NTR (PTS).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: BELONGS TO THE HPR FAMILY.
-----
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-----
DR      EMBL: Z50803; CAA30685.1; -.
DR      HSSP: P08877; 2HPR.
DR      InterPro: IPR001020; HPr_Hisp_site.
DR      InterPro: IPR002114; HPr_Serp_site.
DR      InterPro: IPR000032; HPr_protein.
DR      Pfam: PF00381; PTS-HPR; 1.
DR      PROSITE: PS00369; PTS_HPR_HIS; 1.
DR      PROSITE: PS00589; PTS_HPR_SER; 1.
KW      Phosphotransferase system; Phosphorylation.
FT      MOD_RES 16 16 PHOSPHORYLATION (BY SIMILARITY).
FT      MOD_RES 48 48 PHOSPHORYLATION (BY SIMILARITY).
SQ      SEQUENCE 90 AA: 9820 MW: D5DBD7514B1149C6 CRC64;

Query Match          100.0%; Score 23; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
      |||
DB      29 NYDA 32

RESULT 3
SAA_FELCA STANDARD; PRT; 90 AA.
ID      SAA_FELCA
AC      P19707;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Amyloid protein A (Amyloid fibril protein AA).
OS      Felis silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX      NCBI_TaxID=9685;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=90091422; PubMed=2598632;
RA      Kluge-Beckerman B., Dmilet F.E., Diharbola S.P., Benson M.D.;
RT      "Primary structures of dog and cat amyloid A proteins: comparison to
RT      human AA.";
RL      Comp. Biochem. Physiol. 94B:175-183(1989).
CC      -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC      COMPLEX.
CC      -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC      -1- INDUCTION: UPON CYTOKINE STIMULATION
CC      -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC      EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC      THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS.

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CC      THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC      -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR      PIR: J10111; YICTA.
DR      InterPro: IPR000096; Serum_amyloidA.
DR      Pfam: PF00277; SAA_proteins; 1.
DR      PRINTS: PR00306; SERUMAMYLOID.
DR      ProDom: PD002112; Serum_amyloid_A; 1.
DR      SMART: SM00197; SAA; 1.
DR      PROSITE: PS00992; SAA; 1.
KW      Acute phase; Plasma; HDL; Amyloid.
SQ      SEQUENCE 90 AA: 10122 MW: 112BD4B49B775 CRC64;

Query Match          100.0%; Score 23; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
      |||
DB      40 NYDA 43

RESULT 4
RL23_MYCCA STANDARD; PRT; 94 AA.
ID      RL23_MYCCA
AC      P10140;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-MAR-1989 (Rel. 10, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      50S ribosomal protein L23.
GN      RPLW.
OS      Mycoplasma capricolum.
OC      Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC      Entomoplasmataceae.
OX      NCBI_TaxID=2095;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      STRAIN=ATCC 27343 / KID;
RX      MEDLINE=88142549; PubMed=3481422;
RA      Ohkubo S., Muto A., Kawachi Y., Yamao F., Osawa S.;
RT      "The ribosomal protein gene cluster of Mycoplasma capricolum.";
RL      Mol. Gen. Genet. 210:314-322(1987).
CC      -1- FUNCTION: BINDS TO A SPECIFIC REGION ON THE 23S RNA
CC      (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
-----
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL: X06414; CAA29706.1; -.
DR      PIR: S02833; R51W23.
DR      InterPro: IPR001014; Ribosomal_L23.
DR      Pfam: PF00276; Ribosomal_L23; 1.
DR      ProDom: PD001141; Ribosomal_L23; 1.
DR      PROSITE: PS00050; RIBOSOMAL_L23; 1.
KW      Ribosomal protein; rRNA-binding.
SQ      SEQUENCE 94 AA: 10857 MW: 7D2507D2F1A7FC31 CRC64;

Query Match          100.0%; Score 23; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
      |||
DB      57 NYDA 60

RESULT 5
SAA5_MESAU

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ID SAA5_MESAU STANDARD: PRT: 102 AA.
AC P81491;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Serum amyloid A-5 protein.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP MEDLINE=93294291; PubMed=8515064;
RX de Beer M.C., de Beer F.C., Beach C.M., Connerman W.A., Carreras I.,
RA Spe J.D.;
RT Syrian and Armenian hamsters differ in serum amyloid A gene
RT expression. Identification of novel Syrian hamster serum amyloid A
RT subtypes.";
RL J. Immunol. 150:5361-5370(1993).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR PRODOM: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
DR Acute phase; Plasma; HDL; Amyloid; Multigene family.
KM Acute phase; Plasma; HDL; 8A67FD6852866675 CRC64;
SQ SEQUENCE 102 AA; 11704 MW; 8A67FD6852866675 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
||||
DB 39 NYDA 42

RESULT 6
SAA_HORSE
ID SAA_HORSE STANDARD: PRT: 110 AA.
AC P19857;
DT 01-FEB-1991 (Rel. 17, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serum amyloid A protein (SAA) [Contains: Amyloid protein A (Amyloid
DE fibril protein AA)].
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=89332320; PubMed=2502829;
RA Sletten K., Husebekk A., Husby G.;
RT "The primary structure of equine serum amyloid A (SAA) protein.";
RL Scand. J. Immunol. 30:117-122(1989).
RN [2]
RP SEQUENCE OF 1-80.
RP TISSUE=Liver;
RX MEDLINE=87291864; PubMed=3616485;
RA Sletten K., Husebekk A., Husby G.;
RT "The amino acid sequence of an amyloid fibril protein AA isolated

RT from the horse.";
RL Scand. J. Immunol. 26:79-84(1987).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS
CC FORMED BY THE REMOVAL OF RESIDUES FROM THE CARBOXYL END.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC PIR: A28573; A28573.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR PRODOM: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
KM Acute phase; Plasma; HDL; Amyloid.
FT CHAIN 1 110 SERUM AMYLOID A PROTEIN.
FT CHAIN 1 80 AMYLOID PROTEIN A.
FT VARIANT 16 16 I -> L.
FT VARIANT 44 44 K -> Q.
FT VARIANT 59 59 A -> G.
FT VARIANT 78 78 G -> A.
SQ SEQUENCE 110 AA; 12289 MW; EAE7DBE7AB007E5B CRC64;

Query Match 100.0%; Score 23; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
||||
DB 39 NYDA 42

RESULT 7
SAA_BOVIN
ID SAA_BOVIN STANDARD: PRT: 112 AA.
AC P35841;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serum amyloid A protein (SAA) [Contains: Amyloid protein A (Amyloid
DE fibril protein AA)].
GN SAA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=92150985; PubMed=1738817;
RA Rosevear K., Andresen P.K., Sletten K., Husebekk A., Husby G.,
RA Nordstoga K., Johnson K.H., Westmark G.T., Westmark P.;
RT "The complete amino acid sequence of bovine serum amyloid protein A
RT (SAA) and of subspecies of the tissue-deposited amyloid fibril
RT protein A.";
RL Scand. J. Immunol. 35:217-224(1992).
RN [2]
RP SEQUENCE OF 1-90.
RX MEDLINE=89080450; PubMed=2909653;
RA Benson M.D., Dibatola S.P., Dwulet F.E.;
RT "A unique insertion in the primary structure of bovine amyloid AA
RT protein.";
RL J. Lab. Clin. Med. 113:67-72(1989).
RN [3]
RP SEQUENCE OF 4-16.
RX MEDLINE=88277778; PubMed=3393848;

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RA Husebekk A., Husby G., Sletten K., Skogen B., Nordstoga K.;
RT "Characterization of bovine amyloid proteins SAA and AA.";
RL Scand. J. Immunol. 27:739-743(1988).
RN [4]
RP SEQUENCE OF 3-48.
RX MEDLINE=87079535; PubMed=3791962;
RA Westmark P., Johnson K.H., Westmark G.T., Sletten K., Hayden D.W.;
RT "Bovine amyloid protein AA: Isolation and amino acid sequence
analysis.";
RL Comp. Biochem. Physiol. 85B:609-614(1986).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS
CC FORMED BY THE REMOVAL OF RESIDUES FROM THE CARBOXYL END.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA-proteins; 1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR PRODOM: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
KW Acute phase; Plasma; HDL; Amyloid.
FT CHAIN 1 112 SERUM AMYLOID A PROTEIN.
FT MOD_RES 1 90 AMYLOID PROTEIN A.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SO SEQUENCE 112 AA; 12603 MW; 66E88810D4D49D34 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 112;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
DB 40 NYDA 43

RESULT 8
SAA_SHEEP
ID SAA_SHEEP STANDARD; PRT; 112 AA.
AC P42819;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Serum amyloid A protein (SAA).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=94120345; PubMed=8290897;
RA Syversen P.V., Juul J., Marhaug G., Husby G., Sletten K.;
RT "The primary structure of serum amyloid A protein in the sheep:
Scand. J. Immunol. 39:88-94(1994).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.

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DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA-proteins; 1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR PRODOM: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
KW Acute phase; Plasma; HDL; Amyloid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SO SEQUENCE 112 AA; 12668 MW; 11A37FD59A8C1649 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 112;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
DB 40 NYDA 43

RESULT 9
Y531_BUCAI
ID Y531_BUCAI STANDARD; PRT; 119 AA.
AC P57597;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein B0531.
GN B0531.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. Aps. ";
RL Nature 407:81-86(2000).
CC -1- SIMILARITY: BELONGS TO THE UPF0116 (DSRF) FAMILY.
CC -----
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CC -----
DR EMBL: AP001119; BABI3224.1; -
DR InterPro: IPR003787; DISE.
DR Pfam: PF02635; DsrF; 1.
KW Hypothetical protein; Complete proteome.
SO SEQUENCE 119 AA; 13506 MW; C595F1215BE10938 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 119;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
1111
DB 112 NYDA 115

RESULT 10
SAA1_MESAU
ID SAA1_MESAU STANDARD; PRT; 122 AA.
AC P20726;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Serum amyloid A-1 protein precursor.

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GN SAA1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69352552; PubMed=2765510;
RA Webb C.F., Tucker P.W., Dowton S.B.;
RT "Expression and sequence analyses of serum amyloid A in the Syrian
RL hamster."
CC Biochemistry 28:4785-4790(1989).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
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CC -----
DR EMBL: M27242; AAA37095.1; -.
DR PIR: B30248; B30248.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR ProDom: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
KW Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 122
SQ SEQUENCE 122 AA; 14021 MW; 12F36DB7310A1E68 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. NO. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 59 NYDA 62

RESULT 11
SAAL_MOUSE STANDARD: PRT; 122 AA.
ID SAAL_MOUSE
AC P05366;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serum amyloid A-1 protein precursor.
GN SAA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66250747; PubMed=3013853;
RA Lowell C.A., Potter D.A., Stearnman R.S., Morrow J.F.;
RT "Structure of the murine serum amyloid A gene family. Gene
RL conversion."
J. Biol. Chem. 261:8442-8452(1986).

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RN [2]
RP SEQUENCE OF 9-122 FROM N.A.
RX MEDLINE=85190607; PubMed=3857624;
RA Yamamoto K.-I., Magita S.;
RT "Complete primary structures of two major murine serum amyloid A
RL proteins deduced from cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 82:2915-2919(1985).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13521; AAA40084.1; -.
DR EMBL: M1131; AAA40083.1; -.
DR PIR: A23843; A23843.
DR PIR: A22675; A22675.
DR MGI: 98221; Saa1.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR ProDom: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
KW Acute phase; Plasma; HDL; Signal; Multigene family.
FT SIGNAL 1 19
FT CHAIN 20 122
SQ SEQUENCE 122 AA; 13770 MW; 0AEF6D5F208EAD0 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. NO. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 59 NYDA 62

RESULT 12
SAAL_RABIT STANDARD: PRT; 122 AA.
ID SAAL_RABIT
AC P53614;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Serum amyloid A-1 protein precursor.
GN SAA1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92086827; PubMed=1721234;
RA Rygg M., Marhaug G., Husby G., Dowton S.B.;
RT "Rabbit serum amyloid protein A: expression and primary structure
RL deduced from cDNA sequences."
Scand. J. Immunol. 34:727-734(1991).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;

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CC      THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC      -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: S71722; AAB20616.1.
CC      InterPro: IPR000096; Serum_amyloid_A.
CC      Pfam: PF00277; SAA_proteins; 1.
CC      PRINTS: PR00306; SERUMAMYLOID.
CC      ProDom: PD002112; Serum_amyloid_A; 1.
CC      SMART: SM00197; SAA; 1.
CC      PROSITE: PS00992; SAA; 1.
CC      Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
CC      SIGNAL
CC      CHAIN
CC      SEQUENCE 122 AA; 13655 MW; 98822631B36B2B98 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 122;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NYDA 4
        ||||
Db       59 NYDA 62

RESULT 13
SAA2_MESAU STANDARD: PRT; 122 AA.
ID      SAA2_MESAU
AC      P20727;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Serum amyloid A-2 protein precursor.
GN      SAA2.
OS      Mesocricetus auratus (Golden hamster).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Mesocricetus.
OX      NCBI_TaxID=10036;
[1]
RN      SEQUENCE FROM N.A.
RP      MEDLINE=89352552; PubMed=2765510;
RA      Webb C.F., Tucker P.W., Dowton S.B.;
RT      "Expression and sequence analyses of serum amyloid A in the Syrian
RT      hamster".
RL      Biochemistry 28:4785-4790(1989).
CC      -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC      COMPLEX.
CC      -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC      -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC      -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC      EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC      THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC      THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC      -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC      -----
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CC      -----
CC      EMBL: M27243; AAA37096.1; ALT_SEQ.
CC      PIR: C30248; C30248.

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DR      InterPro: IPR000096; Serum_amyloid_A.
DR      Pfam: PF00277; SAA_proteins; 1.
DR      PRINTS: PR00306; SERUMAMYLOID.
DR      ProDom: PD002112; Serum_amyloid_A; 1.
DR      SMART: SM00197; SAA; 1.
DR      PROSITE: PS00992; SAA; 1.
DR      Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
DR      SIGNAL
DR      CHAIN
DR      SEQUENCE 122 AA; 14110 MW; D99EC964B1C4C22F CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 122;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NYDA 4
        ||||
Db       59 NYDA 62

RESULT 14
SAA2_MOUSE STANDARD: PRT; 122 AA.
ID      SAA2_MOUSE
AC      P05367;
DT      01-NOV-1988 (Rel. 09, Created)
DT      01-NOV-1988 (Rel. 09, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Serum amyloid A-2 protein precursor [Contains: Amyloid protein A
DE      (Amyloid fibril protein AA)].
GN      SAA2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
RN      SEQUENCE FROM N.A.
RP      MEDLINE=86250747; PubMed=3013853;
RA      Lowell C.A., Potter D.A., Stearnan R.S., Morrow J.F.;
RT      "Structure of the murine serum amyloid A gene family. Gene
RT      conversion".
RL      J. Biol. Chem. 261:8442-8452(1986).
[2]
RN      SEQUENCE FROM N.A.
RP      MEDLINE=85190607; PubMed=3857624;
RA      Yamamoto K.-I., Migita S.;
RT      "Complete primary structures of two major murine serum amyloid A
RT      proteins deduced from cDNA sequences".
RL      Proc. Natl. Acad. Sci. U.S.A. 82:2915-2919(1985).
[3]
RN      SEQUENCE OF 32-122 FROM N.A.
RP      MEDLINE=87309776; PubMed=3624868;
RA      Yamamoto K.I., Goto N., Kosaka J., Shiroo M., Yeuil Y.D., Migita S.;
RT      "Structural diversity of murine serum amyloid A genes. Evolutionary
RT      implications".
RL      J. Immunol. 139:1683-1688(1987).
[4]
RN      SEQUENCE OF 20-122.
RP      STRAIN-STL/J;
RC      MEDLINE=92272662; PubMed=1590757;
RA      de Beer M.C., de Beer F.C., Beach C.M., Carreras I., Sipe J.D.;
RT      "Mouse serum amyloid A protein. Complete amino acid sequence and mRNA
RT      analysis of a new isoform".
RL      Biochem. J. 283:673-678(1992).
CC      -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC      COMPLEX.
CC      -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC      -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC      -1- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS
CC      FORMED BY THE REMOVAL OF RESIDUES FROM THE CARBOXYL END.
CC      -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC      EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC      THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC      THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.

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CC -1- MISCELLANEOUS: SAA2 IS THE PREFERRED AMYLOID-FORMING PRECURSOR.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC -----
CC EMBL: M13522; AAA40086.1; -
CC EMBL: M1130; AAA40085.1; -
CC EMBL: M1791; AAA40087.1; -
CC PIR: B23843; B23843.
CC PIR: B22675; B22675.
CC PIR: S21287; S21287.
CC MGD: MGI:98222; Saa2.
CC InterPro: IPR000096; Serum_amyloid_A.
CC Pfam: PF00277; SAA_proteins; 1.
CC PRINTS: PR00306; SERUMAMYLOID.
CC ProDom: PD002112; Serum_amyloid_A; 1.
CC SMART: SM00197; SAA; 1.
CC PROSITE: PS00992; SAA; 1.
CC Acute phase; Plasma; HDL; Amyloid; signal; Multigene family.
CC SIGNAL 1 19
CC CHAIN 20 122 SERUM AMYLOID A-2 PROTEIN.
CC FT CHAIN 20 92 AMYLOID PROTEIN A.
CC FT VARIANT 120 120 A -> D (IN STRAIN SJL/J).
CC SO SEQUENCE 122 AA; 13622 MW; 99E79D6FF97E96B0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 122;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 59 NYDA 62

RESULT 15
SAA2_RABIT
ID SAA2_RABIT STANDARD; PRT; 122 AA.
AC P22000;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Serum amyloid A-2 protein precursor.
GN SAA2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91081342; PubMed=2259638;
RA Tatum F., Alam J., Smith A., Morgan W.T.;
RT "Molecular cloning, nucleotide sequence heterozygosity and regulation
RT of rabbit serum amyloid A cDNA.";
RL Nucleic Acids Res. 18:7447-7447(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91298985; PubMed=1712590;
RA Ray B.K., Ray A.;
RT "Complementary DNA cloning and nucleotide sequence of rabbit serum
RT amyloid A protein.";
RL Biochem. Biophys. Res. Commun. 178:68-72(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92086827; PubMed=1721234;
RA Rygg M., Marhaug G., Husby G., Dowton S.B.;
RT "Rabbit serum amyloid protein A: expression and primary structure

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RT deduced from cDNA sequences.";
RL Scand. J. Immunol. 34:727-734(1991).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
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CC -----
CC EMBL: X16428; CAA34451.1; -
CC EMBL: X16427; CAA34450.1; -
CC EMBL: S71725; AAB20611.1; -
CC PIR: JN0076; JN0076.
CC PIR: S13704; S13704.
CC PIR: S13705; S13705.
CC PIR: S14335; S14335.
CC InterPro: IPR000096; Serum_amyloid_A.
CC Pfam: PF00277; SAA_proteins; 1.
CC PRINTS: PR00306; SERUMAMYLOID.
CC ProDom: PD002112; Serum_amyloid_A; 1.
CC SMART: SM00197; SAA; 1.
CC PROSITE: PS00992; SAA; 1.
CC Acute phase; Plasma; HDL; Amyloid; signal; Multigene family.
CC SIGNAL 1 19
CC CHAIN 20 122 SERUM AMYLOID A-2 PROTEIN.
CC FT CHAIN 20 96 A -> D.
CC FT VARIANT 40 40 S -> T (IN REF. 2).
CC FT CONFLICT 40 40
CC SO SEQUENCE 122 AA; 13451 MW; C135BEF727C57C15 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 122;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 59 NYDA 62

RESULT 16
SAA3_HUMAN
ID SAA3_HUMAN STANDARD; PRT; 122 AA.
AC P22614; O95735;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative serum amyloid A-3 protein.
GN SAA3P OR SAA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128298; PubMed=2558975;
RA Sack G.H. Jr., Talbot C.C. Jr.;
RT "The human serum amyloid A (SAA)-encoding gene SAA1: nucleotide
RT sequence and possible autocatalytic-collagenase-inducer function.";
RL Gene 84:509-515(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92096115; PubMed=1755958;
RA Kluge-Beckerman B., Drumm M.L., Benson M.D.;

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RT "Nonexpression of the human serum amyloid A three (SAA3) gene.";
RL DNA Cell Biol. 10:651-661(1991).
CC -1- FUNCTION: MOST PROBABLY A PSEUDOGENE.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X13895; CAA32096.1; ALT_INIT.
CC EMBL; S73444; -; NOT_ANNOTATED_CDS.
CC PIR; JN0029; JN0029.
CC GeneW; HGNC:10515; SAA3P.
CC InterPro: IPR000096; Serum_amyloid_A.
CC Pfam; PF00277; SAA_proteins; 1.
CC PRINTS; PR00306; SERUMAMYL0ID.
CC PRODOM; PD002112; Serum_amyloid_A; 1.
CC SMART; SM00197; SAA; 1.
CC PROSITE; PS00992; SAA; 1.
CC KM Hypothetical protein.
CC FT CONFLICT 5 T -> Y (IN REF. 2).
CC FT CONFLICT 32 A -> T (IN REF. 2).
CC FT CONFLICT 37 R -> K (IN REF. 2).
CC FT CONFLICT 49 R -> N (IN REF. 2).
CC FT CONFLICT 57 R -> W (IN REF. 2).
CC FT CONFLICT 67 PGG -> LGA (IN REF. 2).
CC SQ SEQUENCE 122 AA; 13440 MW; 70F0BCC052E08472 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   ||||
Db 59 NYDA 62

RESULT 17
SAA3_MESAU STANDARD; PRT; 122 AA.
AC P19453;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Serum amyloid A-3 protein precursor.
GN SAA3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90318412; PubMed=2164641;
RA Gervais C.; Suh M.;
RT "Serum amyloid A protein-related mRNA expression in herpes simplex
RT virus type 2-transformed hamster cells.";
RL Mol. Cell. Biol. 10:4412-4414(1990).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M33431; AAA37098.1; -
CC PIR; A35660; A35660.
CC InterPro: IPR000096; Serum_amyloid_A.
CC Pfam; PF00277; SAA_proteins; 1.
CC PRINTS; PR00306; SERUMAMYL0ID.
CC PRODOM; PD002112; Serum_amyloid_A; 1.
CC SMART; SM00197; SAA; 1.
CC PROSITE; PS00992; SAA; 1.
CC KM Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
CC FT SIGNAL 1 18
CC FT CHAIN 19 122 SERUM AMYLOID A-3 PROTEIN.
CC SQ SEQUENCE 122 AA; 13814 MW; 0DD15D7505518D8A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   ||||
Db 59 NYDA 62

RESULT 18
SAA3_MOUSE STANDARD; PRT; 122 AA.
ID SAA3_MOUSE
AC P04918; Q62201;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serum amyloid A-3 protein precursor.
GN SAA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120372; PubMed=3003697;
RA Stearman R.S.; Lowell C.A.; Peltzman C.G.; Morrow J.F.;
RT "The sequence and structure of a new serum amyloid A gene.";
RL Nucleic Acids Res. 14:797-809(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Swiss;
RX MEDLINE=86250747; PubMed=3013853;
RA Lowell C.A.; Potter D.A.; Stearman R.S.; Morrow J.F.;
RT "Structure of the murine serum amyloid A gene family. Gene
RT conversion.";
RL J. Biol. Chem. 261:8442-8452(1986);
RN [3]
RP SEQUENCE OF 27-64 FROM N.A.
RC STRAIN=BALE/c; TISSUE=Liver;
RX MEDLINE=82229376; PubMed=6953913;
RA Stearman R.S.; Lowell C.A.; Pearson W.R.; Morrow J.F.;
RT "Regulation of synthesis of amyloid A-related protein.";
RL Ann. N.Y. Acad. Sci. 389:106-115(1982).
RN [4]
RP SEQUENCE OF 32-122 FROM N.A.
RX MEDLINE=87309776; PubMed=3624868;
RA Yamamoto K.I.; Goto N.; Kosaka J.; Shiroo M.; Yeul Y.D.; Migita S.;
RT "Structural diversity of murine serum amyloid A genes. Evolutionary
RT implications.";
RL J. Immunol. 139:1683-1688(1987).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES.
CC -----

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CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC -----
DR EMBL: X03479; CAA2719.1; -
DR EMBL: X03505; CAA27219.1; -
DR EMBL: X03506; CAA27219.1; JOINED.
DR EMBL: X03507; CAA27219.1; JOINED.
DR EMBL: M25467; AAA37231.1; -
DR EMBL: M17792; AAA40088.1; -
DR PIR: A23521; A23521.
DR PIR: C23843; C23843.
DR MGD: MGI:98223; Saa3.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS: PR00306; SERUMAMYL0ID.
DR PRODOM: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
KW Acute phase; Plasma; HDL; Signal; Multigene family.
FT SIGNAL 1 19
FT CHAIN 20 122 SERUM AMYLOID A-3 PROTEIN.
FT CONFLICT 57 57 R -> G (IN REF. 4).
SQ SEQUENCE 122 AA; 13773 MW; B9435F82D1B0B705 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4
    ||||
Db 59 NYDA 62

RESULT 19
SAA3_RABIT STANDARD; PRT; 122 AA.
AC P35543;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Serum amyloid A-3 protein precursor.
GN SAA3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91185595; PubMed=1849144;
RA Mitchell T.I., Coon C.T., Brinckerhoff C.E.;
RT "Serum amyloid A (SAA3) produced by rabbit synovial fibroblasts
RT treated with phorbol esters or interleukin 1 induces synthesis of
RT collagenase and is neutralized with specific antiserum.";
RL J. Clin. Invest. 87:1177-1185(1991).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M64696; AAA31464.1; -
DR PIR: S32574; S32574.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS: PR00306; SERUMAMYL0ID.
DR PRODOM: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
KW Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 122 SERUM AMYLOID A-3 PROTEIN.
FT CONFLICT 18 18 BY SIMILARITY.
SQ SEQUENCE 122 AA; 13806 MW; 77E0F502D4284C0B CRC64;

Query Match 100.0%; Score 23; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYDA 4
    ||||
Db 59 NYDA 62

RESULT 20
SAA_HUMAN STANDARD; PRT; 122 AA.
AC P02735; P02736; P02737; Q16879; Q16835.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum amyloid A protein precursor (SAA) [contains: Amyloid protein A
DE (Amyloid fibril protein AA)].
GN SAA1 AND SAA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85252712; PubMed=3839415;
RA Sipe J.D., Colten H.R., Goldberger G., Edge M.D., Tack B.F.,
RA Cohen A.S., Whitehead A.S.;
RT "Human serum amyloid A (SAA): biosynthesis and postsynthetic
RT processing of preSAA and structural variants defined by complementary
RT DNA.";
RL Biochemistry 24:2931-2936(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88058926; PubMed=2890635;
RA Woo P., Sipe J., Dinarello C.A., Colten H.R.;
RT "Structure of a human serum amyloid A gene and modulation of its
RT expression in transfected L cells.";
RL J. Biol. Chem. 262:15790-15795(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87099785; PubMed=3800865;
RA Klive-Beckerman B., Long G.L., Benson M.D.;
RT "DNA sequence evidence for polymorphic forms of human serum amyloid A
RT (SAA)";
RL Biochem. Genet. 24:795-803(1986).
RN [4]
RP SEQUENCE FROM N.A. (SAA1 AND SAA2).
RC TISSUE=Liver;
RX MEDLINE=89034862; PubMed=3183061;
RA Klive-Beckerman B., Dwalet F.E., Benson M.D.;
RT "Human serum amyloid A. Three hepatic mRNAs and the corresponding
RT proteins in one person.";
```

RL J. Clin. Invest. 82:1670-1675(1988).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90262544; PubMed=1971508;
 RA Steinkasserer A., Weiss E.H., Schwaeble W., Linke R.P.;
 RT "Heterogeneity of human serum amyloid A protein. Five different
 RT variants from one individual demonstrated by cDNA sequence
 RT analysis.";
 RL Biochem. J. 268:187-193(1990).
 RN [6]
 RP SEQUENCE FROM N.A. (SAA2 ALPHA).
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 19-122.
 RX MEDLINE=83000248; PubMed=7115671;
 RA Parmelee D.C., Tiltani K., Ericsson L.H., Eriksen N., Benditt E.P.,
 RA Walsh K.A.;
 RT "Amino acid sequence of amyloid-related apoprotein (aposA1) from
 RT human high-density lipoprotein.";
 RL Biochemistry 21:3298-3303(1982).
 RN [8]
 RP SEQUENCE OF 19-122 (VARIANT 1-BETA).
 RX MEDLINE=92189607; PubMed=1546977;
 RA Beech C.M., de Beer M.C., Sipe J.D., Loose L.D., de Beer F.C.;
 RT "Human serum amyloid A protein. Complete amino acid sequence of a new
 RT variant.";
 RL Biochem. J. 282:615-620(1992).
 RN [9]
 RP SEQUENCE OF 20-100.
 RX MEDLINE=88163487; PubMed=3442653;
 RA Prelli F., Pras M., Frangione B.;
 RT "Degradation and deposition of amyloid AA fibrils are tissue
 RT specific.";
 RL Biochemistry 26:8251-8256(1987).
 RN [10]
 RP SEQUENCE OF 19-94 (FAMILIAL MEDITERRANEAN FEVER PATIENT).
 RX MEDLINE=72266653; PubMed=505669;
 RA Levin M., Franklin E.C., Frangione B., Pras M.;
 RT "The amino acid sequence of a major nonimmunoglobulin component of
 RT some amyloid fibrils.";
 RL J. Clin. Invest. 51:2773-2776(1972).
 RN [11]
 RP SEQUENCE OF 19-94 (TUBERCULOSIS PATIENT).
 RX MEDLINE=72266694; PubMed=505786;
 RA Ein D., Kimura S., Terry W.D., Magnocha J., Glenner G.G.;
 RT "Amino acid sequence of an amyloid fibril protein of unknown origin.";
 RL J. Biol. Chem. 247:5653-5655(1972).
 RN [12]
 RP SEQUENCE OF 19-94 (TH).
 RX MEDLINE=74120351; PubMed=4816450;
 RA Sletten K., Husby G.;
 RT "The complete amino-acid sequence of non-immunoglobulin amyloid
 RT fibril protein AS in rheumatoid arthritis.";
 RL Eur. J. Biochem. 41:117-123(1974).
 RN [13]
 RP SEQUENCE OF 19-82 (JL).
 RX MEDLINE=76160745; PubMed=1259755;
 RA Sletten K., Husby G., Natvig J.B.;
 RT "The complete amino acid sequence of an amyloid fibril protein AAI of
 RT unusual size (64 residues).";
 RL Biochem. Biophys. Res. Commun. 69:19-25(1976).
 RN [14]
 RP SEQUENCE OF 19-101 (BOL).
 RX MEDLINE=80213686; PubMed=6155694;
 RA Moyner K., Sletten K., Husby G., Natvig J.B.;
 RT "An unusually large (83 amino acid residues) amyloid fibril protein
 RT amyloidosis.";
 RL Scand. J. Immunol. 11:549-554(1980).
 RN [15]

RP SEQUENCE OF 19-42.
 RA Benditt E.P., Eriksen N., Hermanson M.A., Ericsson L.H.;
 RT "The major proteins of human and monkey amyloid substance: common
 RT properties including unusual N-terminal amino acid sequences.";
 RL Fests Lett. 19:169-173(1971).
 RN [16]
 RP SEQUENCE OF 32-122 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92022342; PubMed=1656519;
 RA Belts J., Edbrooke M., Thakker R.,
 RT "The human acute-phase serum amyloid A gene family: structure,
 RT evolution and expression in hepatoma cells.";
 RL Scand. J. Immunol. 34:471-482(1991).
 RN [17]
 RP VARIANT 1-GAMMA.
 RX MEDLINE=93290347; PubMed=8512321;
 RA Baba S., Takahashi T., Kasama T., Fujie M., Shirasawa H.;
 RT "A novel polymorphism of human serum amyloid A protein, SAA1 gamma,
 RT is characterized by alanines at both residues 52 and 57.";
 RL Arch. Biochem. Biophys. 303:361-366(1993).
 RN [18]
 RP PARTIAL SEQUENCE (VARIOUS ISOFORMS), AND METHYLATION OF ASN-101.
 RX MEDLINE=96377164; PubMed=8783012;
 RA Ducret A., Bruun C.F., Bures E.J.,
 RA Aebbersold R.;
 RT "Characterization of human serum amyloid A protein isoforms separated
 RT by two-dimensional electrophoresis by liquid
 RT chromatography/electrospray ionization tandem mass spectrometry.";
 RL Electrophoresis 17:866-876(1996).
 CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLOPROTEIN OF THE HDL
 CC COMPLEX.
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
 CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
 CC -1- PPM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS
 CC FORMED BY THE REMOVAL OF APPROXIMATELY 24 RESIDUES FROM THE
 CC CARBOXYL END.
 CC -1- POLYMORPHISM: BOTH SAA1 AND SAA2 HAVE A NUMBER OF ALLELES. WE USE
 CC HERE THE NOMENCLATURE OF REF.6. THE SEQUENCE SHOWN IS THAT OF
 CC 1-ALPHA.
 CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
 CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
 CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
 CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
 CC -1- DISEASE: BOL IS FROM A PATIENT WITH WALDENSTROM'S
 CC MACROGLOBULINEMIA.
 CC -1- DISEASE: JL IS FROM A PATIENT WITH ANKYLOSING SPONDYLITIS.
 CC -1- DISEASE: TH IS FROM A PATIENT WITH JUVENILE RHEUMATOID ARTHRITIS.
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
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 CC -----
 DR EMBL: M10906; AAA60297.1; -
 DR EMBL: J03474; AAB59539.1; -
 DR EMBL: M23698; AAA64799.1; -
 DR EMBL: M23699; AAA64800.1; -
 DR EMBL: M26152; AAA85338.1; -
 DR EMBL: BC020795; AAH20795.1; -
 DR EMBL: X51439; CAA35804.1; -
 DR EMBL: X51440; CAA35805.1; -
 DR EMBL: X51441; CAA35806.1; -
 DR EMBL: X51442; CAA35807.1; -
 DR EMBL: X51443; CAA35808.1; -
 DR EMBL: X51444; CAA35809.1; -
 DR EMBL: X51445; CAA35810.1; -
 DR EMBL: X56653; CAA39975.1; -
 DR PIR: A03195; YLH05.
 DR PIR: A03196; YLH0TH.
 DR PIR: A03197; YLH0A.

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DR PIR: A22342; A22342.
DR PIR: A27902; A27902.
DR PIR: A28445; A28445.
DR PIR: A29419; A29419.
DR PIR: S09972; S09972.
DR PIR: S09973; S09973.
DR PIR: S09974; S09974.
DR PIR: S09975; S09975.
DR PIR: S09976; S09976.
DR PIR: S09977; S09977.
DR PIR: S09978; S09978.
DR Genew; HGNC:10513; SAA1.

Query Match          100.0%; Score 23; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   |||
Db 59 NYDA 62

RESULT 21
SAA_ANAPL STANDARD: PRT; 127 AA.
AC P02740; 092034;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serum amyloid A protein precursor (SAA).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Pekin breed; TISSUE=Liver;
RX MEDLINE-97121423; Pubmed-8962089;
RA Guo J.T., Aldrich C., Mason W.S., Pugh J.C.;
RT "Characterization of serum amyloid A protein mRNA expression and
RT secondary amyloidosis in the domestic duck.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14548-14553(1996).
RN [2]
RP SEQUENCE OF 19-124.
RX MEDLINE-87247238; Pubmed-3109944;
RA Ericsson L.H., Eriksen N., Walsh K.A., Benditt E.P.;
RT "Primary structure of duck amyloid protein A. The form deposited in
RT tissues may be identical to its serum precursor.";
RL PERS Lett. 218:11-16(1987).
RN [3]
RP SEQUENCE OF 19-99.
RX MEDLINE-77142518; Pubmed-845435;
RA Gorevic P.D., Greenwald M., Frangione B., Pras M., Franklin E.C.;
RT "The amino acid sequence of duck amyloid A (AA) protein.";
RL J. Immunol. 118:1113-1118(1977).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC ALSO PRESENT IN THE LIVER AND LUNG IRRESPECTIVE OF INDUCTION.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN AA, WHICH
CC IS FORMED BY THE REMOVAL OF APPROXIMATELY 3 RESIDUES FROM THE
CC CARBOXYL END.
CC -1- POLYMORPHISM: AT LEAST TWO ALLELES EXIST. THE SEQUENCE OF THE
CC B ALLELE IS SHOWN HERE.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC -----
DR EMBL; U59909; AAC60058.1; -
DR EMBL; U59908; AAC60057.1; -
DR EMBL; U64985; AAC60059.1; -
DR PIR; A03200; YLDKA.
DR PIR; A27227; A27227.
DR PIR; A32538; A32538.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYLOID.
DR Prodom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; Plasma; HDL; Amyloid; Signal.
FT SIGNAL 1 18
FT CHAIN 19 127 SERUM AMYLOID A PROTEIN.
FT VARIANT 89 89 G -> S (IN ALLELE A).
FT VARIANT 107 107 A -> V (IN ALLELE A).
FT CONFLICT 81 82 SD -> AN (IN REF. 3).
FT CONFLICT 93 93 MISSING (IN REF. 3).
FT CONFLICT 99 99 T -> R (IN REF. 3).
SQ SEQUENCE 127 AA; 13873 MW; 6F61476AEAB9EB6F CRC64;

Query Match          100.0%; Score 23; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   |||
Db 63 NYDA 66

RESULT 22
SAA_MACEU STANDARD: PRT; 127 AA.
AC P53613;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Serum amyloid A protein precursor (SAA).
DE Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE-96179383; Pubmed-8602460;
RA Uhlar C.M., Black I.L., Shields D.C., Brack C.M., Schreiber G.,
RA Whitehead A.S.;
RT "Wallaby serum amyloid A protein: cDNA cloning, sequence and
RT evolutionary analysis.";
RL Scand. J. Immunol. 43:271-276(1996).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U39363; AAB02187.1; -

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DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins: 1.
DR PRINTS: PR00306; SERUMAMYL0ID.
DR ProDom: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
DR Acute phase; Plasma; HDL; Signal.
FT SIGNAL 1 18
FT CHAIN 19 127
FT METAL 121 121
SQ SEQUENCE 127 AA; 14322 MW; D2405776418F4FB CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 127;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 63 NYDA 66

RESULT 23
CYCP_RHOSP STANDARD; PRT; 128 AA.
ID CYCP_RHOSP
AC P00146;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Cytochrome c'.
DE Cytochrome c'.
OS Rhodospseudomonas sp.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Rhodospseudomonas.
OX NCBI_TaxID=1078;
RN [1]
RP SEQUENCE.
RC STRAIN=TJ12;
RA MEDLINE=82082545; PubMed=6273892;
RA Ambler R.P., Bartsch R.G., Daniel M., Kamen M.D., McElellan L.,
Meyer T.E., van Beumen J.;
RT "Amino acid sequences of bacterial cytochromes c' and c-556.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:6854-6857(1981).
CC -I- FUNCTION: CYTOCHROME C' IS THE MOST WIDELY OCCURRING BACTERIAL
C-TYPE CYTOCHROME. CYTOCHROMES C' ARE HIGH-SPIN PROTEINS AND THE
CC HEME HAS NO SIXTH LIGAND. THEIR EXACT FUNCTION IS NOT KNOWN.
CC PIR: A00139; CCRCCX.
DR HSP: P00147; ICPO.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR002321; Cyt_CII.
DR Pfam: PF01322; Cytochrome_C_2; 1.
DR PRINTS: PR00608; CYTCHROME_CII.
DR ProDom: PD003828; Cyt_CII; 1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme.
FT BINDING 117 117
FT BINDING 120 120
FT METAL 121 121
FT METAL 121 121
SQ SEQUENCE 128 AA; 13371 MW; F49957285708124F CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 128;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 29 NYDA 32

RESULT 24
SAA1_MUSVI STANDARD; PRT; 129 AA.
ID SAA1_MUSVI
AC P18575;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

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DE Serum amyloid A-1 protein precursor.
GN SAA1.
OS Musstela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90277614; PubMed=2351648;
RA Marhang G., Husby G., Downton S.B.;
RT "Mink serum amyloid A protein. Expression and primary structure based
on cDNA sequences.";
RL J. Biol. Chem. 265:10049-10054(1990).
CC -I- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
COMPLEX.
CC -I- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -I- INDUCTION: UPON CYTOKINE STIMULATION.
CC -I- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -I- MISCELLANEOUS: SAA2 IS MORE AMYLOIDOGENIC THAN SAA1.
CC -I- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M34953; AAA30968.1; -.
DR PIR: A36451; A36451.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins: 1.
DR PRINTS: PR00306; SERUMAMYL0ID.
DR ProDom: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
DR Acute phase; Plasma; HDL; Amyloid; Signal; Multigene family.
KW SIGNAL 1 18
FT CHAIN 19 129
FT MOD_RES 19 19
FT MOD_RES 19 19
SQ SEQUENCE 129 AA; 14389 MW; D73D3DD95519E068 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 129;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 58 NYDA 61

RESULT 25
SAA2_MUSVI STANDARD; PRT; 129 AA.
ID SAA2_MUSVI
AC P02739;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serum amyloid A-2 protein precursor [Contains: Amyloid protein A
(Amyloid fibril protein AA)].
GN SAA2.
OS Musstela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90277614; PubMed=2351648;
RA Marhaug G., Husby G., Dowton S.B.;
RT "Mink serum amyloid A protein. Expression and primary structure based
RL on cDNA sequences.";
RN J. Biol. Chem. 265:10049-10054(1990).
[2]
RP SEQUENCE OF 19-82.
RX MEDLINE=80156813; PubMed=6767608;
RA Waalen K., Sletten K., Husby G., Nordstoga K.;
RT "The primary structure of amyloid fibril protein AA in
RL endotoxin-induced amyloidosis of the mink.";
RN Eur. J. Biochem. 104:407-412(1980).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- MISCELLANEOUS: SAA2 IS MORE AMYLOIDOGENIC THAN SAA1.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
-----
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-----
DR EMBL; M34954; AAA30969.1; -
DR PIR; A03199; YLMAA.
DR EMBL; B36451; B36451.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYLOID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
DR Acute phase; Plasma; HDL; Amyloid; signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 129 SERUM AMYLOID A-2 PROTEIN.
FT CHAIN 19 82 AMYLOID PROTEIN A.
FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
FT VARIANT 24 24 I -> F.
FT VARIANT 24 24
SQ SEQUENCE 129 AA; 14456 MW; B79402006B34B882 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
DB 58 NYDA 61

RESULT 26
SAA_CANFA STANDARD; PRT; 129 AA.
AC P19708;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serum amyloid A protein precursor (SAA) [contains: Amyloid protein A
DE (Amyloid fibril protein AA)].
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=91139635; PubMed=1995613;
RA Sellar G.C., Debeer M.C., Lelias J.M., Snyder P.W., Glickman L.T.,
RA Feisburg P.J., Whitehead A.S.;
RT "Dog serum amyloid A protein. Identification of multiple isoforms
RL defined by cDNA and protein analyses.";
RN J. Biol. Chem. 266:3505-3510(1991).
[2]
RP SEQUENCE OF 19-111.
RX MEDLINE=90091422; PubMed=2598632;
RA Kluge-Beckerman B., Dwulet F.E., Dibatola S.P., Benson M.D.;
RT "Primary structures of dog and cat amyloid A proteins: comparison to
RL human AA.";
RN Comp. Biochem. Physiol. 94B:175-183(1989).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.
CC -1- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS
CC FORMED BY THE REMOVAL OF RESIDUES FROM THE CARBOXYL END.
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
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DR EMBL; M59171; AAA62762.1; -
DR EMBL; M59172; AAA62763.1; -
DR EMBL; M59173; AAA62764.1; -
DR EMBL; M59174; AAA62765.1; -
DR EMBL; M59175; AAA51457.1; -
DR PIR; J10110; YLDGA.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYLOID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
DR Acute phase; Plasma; HDL; Amyloid; Multigene family; signal;
FT SIGNAL 1 18
FT CHAIN 19 129 SERUM AMYLOID A PROTEIN.
FT CHAIN 19 111 AMYLOID PROTEIN A.
FT PROPSP 112 129 OFTEN CLEAVED DURING AMYLOIDOGENESIS.
FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
FT VARIANT 25 25 S -> G.
FT VARIANT 35 35 W -> L.
FT VARIANT 88 90 LTR -> RLK.
SQ SEQUENCE 129 AA; 14339 MW; 91B21ACBA1F998C9 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
| | | |
DB 58 NYDA 61

RESULT 27
SAA4_HUMAN STANDARD; PRT; 130 AA.
AC P35542;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

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16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serum amyloid A-4 protein precursor (Constitutively expressed serum
 DE amyloid A protein) (C-SAA).
 GN SAA4 OR CSAA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92156125; PubMed=1740433;
 RA Whitehead A.S., Debeer M.C., Steel D.M., Rits M., Lelias J.M.,
 RA Lane W.S., Debeer F.C.;
 RT "Identification of novel members of the serum amyloid A protein
 RT superfamily as constitutive apolipoproteins of high density
 RT lipoprotein.";
 RL J. Biol. Chem. 267:3862-3867(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93300520; PubMed=7686132;
 RA Steel D.M., Sellar G.C., Uhlar C.M., Simon S., Debeer F.C.,
 RA Whitehead A.S.;
 RT "A constitutively expressed serum amyloid A protein gene (SAA4) is
 RT closely linked to, and shares structural similarities with, an acute-
 RT phase serum amyloid A protein gene (SAA2).";
 RL Genomics 16:447-454(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93068025; PubMed=1439582;
 RA Watson G., Coade S., Woo P.;
 RT "Analysis of the genomic and derived protein structure of a novel
 RT human serum amyloid A gene, SAA4.";
 RL Scand. J. Immunol. 36:703-712(1992).
 RN [4]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=96371164; PubMed=8783012;
 RA Ducret A., Bruun C.F., Bures E.J., Marhaug G., Husby G.,
 RA Aebbersold R.;
 RT "Characterization of human serum amyloid A protein isoforms separated
 RT by two-dimensional electrophoresis by liquid
 RT chromatography/electrospray ionization tandem mass spectrometry.";
 RL Electrophoresis 17:866-876(1996).
 CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 CC COMPLEX.
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
 CC -1- INDUCTION: CONSTITUTIVELY EXPRESSED.
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
 CC -----
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 CC -----
 DR EMBL: S48883; AAB24060.1; .
 DR EMBL: S48980; AAB24060.1; JOINED.
 DR EMBL: S48981; AAB24060.1; JOINED.
 DR EMBL: L05920; .; NOT ANNOTATED_CDS.
 DR EMBL: M81349; AAB60258.1; .
 DR PIR: A42258; A42258.
 DR Genew: HGNC:10516; SAA4.
 DR MIM: 104752; .
 DR InterPro: IPR000096; Serum_amyloid_A.
 DR Pfam: PF00277; SAA_proteins.1.
 DR PRINTS: PR00306; SERUMAMYLID.
 DR PRODOM: PD002112; Serum_amyloid_A.1.
 DR SMART: SM00197; SAA.1.
 DR PROSITE: PS00992; SAA.1.
 KW Acute phase; Plasma; HDL; Signal; Multigene family; Glycoprotein.
 FT SIGNAL 1 18

FT CHAIN 19 130 SERUM AMYLOID A-4 PROTEIN.
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (PARTIAL).
 SQ SEQUENCE 130 AA; 14807 MW; 0F86E9F1EF00B1C CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 130;
 Best local Similarity 100.0%; Pred. No. 64;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 NYDA 4
 DB 59 NYDA 62
 RESULT 28
 COAC_HUMAN STANDARD; PRT; 142 AA.
 AC Q14019;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coactosin-like protein.
 GN CLP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Placenta;
 RA Chen K.-S., Manian P., Koeuth T., Potocki L., Zhao Q., Chinault A.C.,
 RA Lee C.-C., Lupski J.R.;
 RT "Homologous recombination of a flanking repeat gene cluster is a
 RT mechanism for a common contiguous gene deletion syndrome.";
 RL Nat. Genet. 17:154-163(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, Lung, and Uterus;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MUTAGENESIS OF
 RP LYS-75.
 RP PubMed=11583571;
 RA Provost P., Doucet J., Stock A., Gerisch G., Samuelsson B.,
 RA Radmark O.;
 RT "Coactosin-like protein, a human F-actin-binding protein: critical
 RT role of lysine-75.";
 RL Biochem. J. 359:255-263(2001).
 RN [4]
 RP INTERACTION WITH 5-LIPOXYGENASE, AND MUTAGENESIS OF LYS-130 AND
 RP LYS-131.
 RP PubMed=11297527;
 RA Provost P., Doucet J., Hammarberg T., Gerisch G., Samuelsson B.,
 RA Radmark O.;
 RT "5-Lipoxygenase interacts with coactosin-like protein.";
 RL J. Biol. Chem. 276:16520-16527(2001).
 CC -1- FUNCTION: Binds to F-actin in a calcium-independent manner. Has no
 CC direct effect on actin depolymerization.
 CC -1- SUBUNIT: Interacts with 5-lipoxygenase (5LO) in a calcium-
 CC independent manner.
 CC TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC placenta, lung, kidney and peripheral blood leukocytes and lower
 CC levels in brain, liver and pancreas.
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
 CC COACTOSIN SUBFAMILY.
 CC -----
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CC      riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
CC      -1- PATHWAY: Riboflavin biosynthesis; last step.
CC      -1- SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
CC      -----
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CC      -----
DR      EMBL; M90094; AAA73230.1; -.
DR      PIR; PC1110; PC1110.
DR      HSSP; P11998; IRVY.
DR      InterPro; IPR002180; DMRL_synthase.
DR      Pfam; PF00885; DMRL_synthase; 1.
DR      ProDom; PD003664; DMRL_synthase; 1.
DR      TIGRFAMs; TIGR00114; ribH; 1.
DR      TIGRFAMs; TIGR00114; ribH; 1.
KW      Riboflavin biosynthesis; transferase.
FT      NON_TER
SQ      SEQUENCE 144 AA; 144 MW; 4A4E4820CD960359 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 144;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
Db      71 NYDA 74

RESULT 31
RISB_STAM
ID      RISB_STAM STANDARD; PRT; 154 AA.
AC      093188; 099TAL;
DT      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
DE      6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
DE      (Lumazine synthase) (Riboflavin synthase beta chain).
GN      RIBH OR SAV1767 OR SA1586 OR MM1708.
OS      Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS      Staphylococcus aureus (strain N315) / and
OS      Staphylococcus aureus (strain MW2).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=158878, 158879, 196620;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Mu50 / ATCC 700699, and N315;
RC      MEDLINE=21311952; PubMed=11418146;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian Y.-O., Ito T.,
RA      Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA      Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA      Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA      Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA      Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus";
RL      Lancet 357:1225-1240(2001).
RP      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-MW2;
RC      MEDLINE=22040717; PubMed=12044378;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA      Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA      Yamamoto K., Hiramatsu K.;
RT      "Genome and virulence determinants of high virulence community-
RT      acquired MRSA";
RL      Lancet 359:1819-1827(2002).
CC      -1- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
CC      catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-

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CC      ribityl-amino-2,4(1H,3H)-pyrimidinone and U-3,4-dihydroxy-2-
CC      butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
CC      catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-
CC      2,4(1H,3H)-pyrimidinone with U-3,4-dihydroxy-2-butanone-4-
CC      phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).
CC      -1- CATALYTIC ACTIVITY: 6,7-dimethyl-8-(1-D-ribityl)lumazine =
CC      riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
CC      -1- PATHWAY: Riboflavin biosynthesis; last step.
CC      -1- SIMILARITY: BELONGS TO THE DMRL SYNTHASE FAMILY.
CC      -1- CAUTION: Rel.1 strain Mu50 sequence differs from that shown due to
CC      a frameshift in position 28.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; AP003363; BAB57929.1; ALT_FRAME.
DR      EMBL; AP003363; BAB42854.1; -.
DR      EMBL; AP004828; BAB95573.1; -.
DR      InterPro; IPR002180; DMRL_synthase.
DR      Pfam; PF00885; DMRL_synthase; 2.
DR      ProDom; PD003664; DMRL_synthase; 1.
DR      TIGRFAMs; TIGR00114; ribH; 1.
KW      Riboflavin biosynthesis; transferase; Complete proteome.
SQ      SEQUENCE 154 AA; 16410 MW; BC6AD39B6431BF44 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 154;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYDA 4
Db      70 NYDA 73

RESULT 32
FMF5_ECOLI
ID      FMF5_ECOLI STANDARD; PRT; 159 AA.
AC      P13719;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      F1845 fimbrial protein precursor (Fimbrial adhesin F1845 antigen).
DE      F1845 fimbrial protein precursor (Fimbrial adhesin F1845 antigen).
GN      DAAE.
OS      Escherichia coli.
OS      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C1845;
RC      MEDLINE=89327142; PubMed=2568985;
RA      Bilge S.S., Clausen C.R., Lau W., Moseley S.L.;
RA      "Molecular characterization of a fimbrial adhesin, F1845, mediating
RT      diffuse adherence of diarrhea-associated Escherichia coli to HEp-2
RT      cells";
RL      J. Bacteriol. 171:4281-4289(1989).
RP      [2]
RP      FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC      FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC      MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC      COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC      -1- SUBCELLULAR LOCATION: Fimbria.
CC      -1- DISEASE: HEMAGGLUTININS OF UROPATHOGENIC E. COLI MEDIATE ADHERENCE
CC      TO THE UPPER URINARY TRACT. THESE ADHESINS BIND TO THE DR BLOOD
CC      GROUP ANTIGEN AND ALSO AGGLUTINATE HUMAN ERYTHROCYTES IN THE
CC      PRESENCE OF D-MANNOSE (MANNOSE-RESISTANT HEMAGGLUTINATION (MRA)).
CC      -1- DISEASE: C1845 IS A STRAIN RESPONSIBLE FOR DIARRHEAL DISEASE.
CC      -1- SIMILARITY: BELONGS TO THE AFA-I/AFA-III/DRAA/DAAE FAMILY OF
CC      ADHESINS.

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CC -----
DR EMBL; M27725; AAA23661.1; -
DR PIR; A33859; A33859.
KW Fimbrin; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 159
SQ SEQUENCE 159 AA; 16722 MW; ABC240A2DB65C2ED CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 159;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 85 NYDA 88

RESULT 33
UBCG_SCHPO STANDARD: PRT; 160 AA.
ID UBCG_SCHPO
AC O9P611;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable ubiquitin-conjugating enzyme E2-17 kDa (EC 6.3.2.19)
DE (Ubiquitin-protein ligase) (Ubiquitin carrier protein).
GN UBC16 OR SPBC1198.09.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brookes K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer D., Hilbert A.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehnach R., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT *The genome sequence of Schizosaccharomyces pombe.*
RL Nature 415:871-880(2002).
CC -1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
CC PROTEINS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine - AMP +

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CC -----
DR EMBL; M27725; AAA23661.1; -
DR PIR; A33859; A33859.
KW Fimbrin; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 159
SQ SEQUENCE 159 AA; 16722 MW; ABC240A2DB65C2ED CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 160;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 117 NYDA 120

RESULT 34
TPX_STRPA STANDARD: PRT; 163 AA.
ID TPX_STRPA
AC P31307;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable thiol peroxidase (EC 1.11.1.-).
GN TPX.
OS Streptococcus parvaanguis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1318;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FW213;
RX MEDLINE=90035427; PubMed=2572555;
RA Fenu J.C., Leblanc D.J., Flves-Taylor P.,
RT *Nucleotide sequence analysis of a type 1 fimbrial gene of
RT Streptococcus sanguis FW213.*
RL Infect. Immun. 57:3527-3533(1989).
CC -1- FUNCTION: HAS ANTIOXIDANT ACTIVITY. COULD REMOVE PEROXIDES OR
CC H(2O(2)) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHP/TSA FAMILY. TPX SUBFAMILY.
CC -----
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CC -----
DR EMBL; M26130; AAA53078.1; -
DR InterPro; IPR000865; AhpC-TSA.
DR InterPro; IPR002065; TPX.
DR Pfam; PF00578; AhpC-TSA; 1.
DR PROSITE; PS01265; TPX; 1.

```

KW Oxidoreductase; Peroxidase.
 FT INIT_MER 0 BY SIMILARITY.
 SQ SEQUENCE 163 AA; 17825 MW; E731B812D772CBAA CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 DB 151 NYDA 154

RESULT 35
 PHA2_SYNPY STANDARD; PRT; 165 AA.
 ID PHA2_SYNPY
 AC P27646;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-phycocerythrin class II alpha chain.
 GN MPEA.
 OS Synechococcus sp. (strain WH8020).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=32052;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93144698; PubMed=8425055;
 RA de Lorimier R., Wilbanks S.M., Glazer A.N.;
 RT "Genes of the R-phycocyanin II locus of marine Synechococcus spp.,
 RT and comparison of protein-chromophore interactions in phycocyanins
 RT differing in bilin composition.";
 RL Plant Mol. Biol. 21:225-237(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91236722; PubMed=1903390;
 RA Wilbanks S.M., de Lorimier R., Glazer A.N.;
 RT "Phycocerythrins of marine unicellular cyanobacteria. III. Sequence of
 RT a class II phycocerythrin.";
 RL J. Biol. Chem. 266:9535-9539(1991).
 RN [3]
 RP CHROMOPHORES, AND PARTIAL SEQUENCE.
 RX MEDLINE=91236720; PubMed=1903388;
 RA Ong L.U., Glazer A.N.;
 RT "Phycocerythrins of marine unicellular cyanobacteria. I. Bilin types
 RT and locations and energy transfer pathways in Synechococcus spp.
 RT phycocerythrins.";
 RL J. Biol. Chem. 266:9515-9527(1991).
 CC -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
 CC FROM THE PHYCOBILIPROTEIN COMPLEX.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Periphery of the rods of the phycobillosome.
 CC -1- PTM: CONTAINS THREE COVALENTLY LINKED BILIN CHROMOPHORES.
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 CC -----
 CC EMBL, M5288; AAA27333.1; -
 CC EMBL, M6118; AAA27320.1; -
 CC PIR, A40007; A40007.
 CC PIR, S31048; S31048.
 CC HSP, O36005; 1B8D.
 CC InterPro: IPR001859; Phycobillosome.
 CC Pfam: PF00502; Phycobillosome; 1.
 CC ProDom: PD000340; Phycobillosome; 1.
 KW Phycobillosome; Election transport; Photosynthesis; Bile pigment.
 FT BINDING 75 75 PHYCOBILIPROTEIN CHROMOPHORE.
 FT BINDING 83 83 PHYCOERYTHROBILIN CHROMOPHORE 1.

FT BINDING 140 140 PHYCOERYTHROBILIN CHROMOPHORE 2.
 SQ SEQUENCE 165 AA; 17670 MW; B17A9C0B45D24602 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 DB 47 NYDA 50

RESULT 36
 TPX_PASMU STANDARD; PRT; 165 AA.
 ID TPX_PASMU
 AC P57880;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable thiol peroxidase (EC 1.11.1.-).
 GN TPX OR PM0820.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida PM70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- FUNCTION: HAS ANTIOXIDANT ACTIVITY. COULD REMOVE PEROXIDES OR
 CC H(2)O(2) (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TPX SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL, AE006121; AAK02904.1; -
 CC InterPro: IPR000866; Ahpc-TSA.
 CC InterPro: IPR002065; TPX.
 CC Pfam: PF00578; Ahpc-TSA; 1.
 CC PROSITE: PS01265; TPX; 1.
 KW Oxidoreductase; Peroxidase; Complete proteome.
 SQ SEQUENCE 165 AA; 17706 MW; 21A6EBA9B9A11C7 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 DB 157 NYDA 160

RESULT 37
 WRBA_ECO57 STANDARD; PRT; 197 AA.
 ID WRBA_ECO57
 AC O8X4B4; O8X468; O9KXH7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Flavoprotein wrba (Tfp repressor binding protein).
 GN WRBA OR Z1423/Z1504 OR ECS1159.1/ECS1251.1.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.

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0X NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=20198780; PubMed=10734605;
RA Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kimura S.,
RA Kurokawa K., Ishii K., Hattori M., Tatsuno I., Abe H., Iida T.,
RA Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Honda T.,
RA Sasaoka C., Shinagawa H.;
RT "Complete nucleotide sequence of the prophage VT2-Sakai carrying the
RT verotoxin 2 genes of the enterohaemorrhagic Escherichia coli O157:H7
RT derived from the Sakai outbreak.";
RL Genes Genet. Syst. 74:227-239(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimelanta E.T., Potamocus K.,
RA Apodaca J., Anantharaman T.S., Ian J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Y.,
RA Iida T., Takami H., Honda T., Sasaoka C., Ogasawara N., Yasunaga T.,
RA Kunita S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -I- FUNCTION: Seems to enhance the formation and/or stability of
CC noncovalent complexes between the trp repressor protein and
CC operator-bearing DNA (By similarity).
CC -I- COFACTOR: Binds 1 FMN per monomer (By similarity).
CC -I- SIMILARITY: BELONGS TO THE WRBA FAMILY.
CC -I- CAUTION: WRBA is interrupted by the insertion of the prophage VT2-
CC Sakai between positions 17 and 18.
CC -----
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CC -----
DR EMBL: AP000422; BAA94098.1; -
DR EMBL: AE005284; AAG55552.1; ALT_INIT.
DR EMBL: AE005300; AAG55621.1; ALT_TERM.
DR EMBL: AP002554; -; NOT_ANNOTATED_CDS.
DR InterPro: IPR001226; Flavodoxin.
DR Pfam: PF00258; Flavodoxin; 1.
DR PROSITE: PS00201; FLAVODOXIN; FALSE_NEG.
DR Flavoprotein; FMN; Complete proteome.
KM INIT_MET 0 0 BY SIMILARITY.
SQ SEQUENCE 197 AA; 20703 MW; 7117EF933B72447 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. NO. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYDA 4
| | | |
Db 67 NYDA 70

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ID	YCP2_PSEB9	STANDARD:	PRT:	202 AA.
AC	P29300;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	01-APR-1993 (Rel. 25, Last annotation update)			
DE	Hypothetical phycocyanin operon protein Z (ORF Z).			
OS	<i>Pseudanabaena</i> sp. (strain PCC 7409).			
OC	<i>Bacteria</i> ; <i>Cyanobacteria</i> ; <i>Oscillatoriales</i> ; <i>Pseudanabaena</i> .			
OX	NCBI_TaxID=29415;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92236425; PubMed=1809846;			
RA	Dubbs J.M., Bryant D.A.;			
RT	"Molecular cloning and transcriptional analysis of the <i>cpeB</i> operon			
RT	of the cyanobacterium <i>Pseudanabaena</i> species PCC7409."			
RL	Mol. Microbiol. 5:3073-3085(1991).			
CC	-1- INDUCTION: PRESENT IN BOTH RED- AND GREEN-LIGHT-GROWN CELLS.			
CC	-1- SIMILARITY: TO ITS CALOTHRIX SP. PCC 7601 HOMOLOG.			
CC	-----			
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CC	-----			
DR	EMBL: X63073; CAA44797.1; -.			
DR	PIR: S18528; S18528.			
DR	InterPro: IPR004155; PBS_lyase_HEAT.			
DR	Pfam: PF03130; HEAT_PBS; 3.			
DR	Hypothetical protein; Phycobilisome.			
SO	SEQUENCE 202 AA; 21516 MW; B875183B15E4FF94 CRC64;			
Query Match 100.0%; Score 23; DB 1; Length 202;				
Best Local Similarity 100.0%; Pred. NO. 1e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 NYDA 4			
DB	28 NYDA 31			
RESULT 39				
Y363_LISMO				
ID	Y363_LISMO	STANDARD:	PRT:	205 AA.
AC	P58495;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Probable peptidase Lmo0363 (EC 3.4.-.-).			
GN	LMO0363.			
OS	<i>Listeria</i> monocytogenes.			
OC	<i>Bacteria</i> ; <i>Firmicutes</i> ; <i>Bacillales</i> ; <i>Listeriaceae</i> ; <i>Listeria</i> .			
OX	NCBI_TaxID=1639;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-EGD- / Serovar 1/2a;			
RX	MEDLINE=21537279; PubMed=11679669;			
RA	Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,			
RA	Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,			
RA	Charbit A., Cheounani F., Couve E., de Darvar A., Dehoux P.,			
RA	Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,			
RA	Entian K.-D., Fshl H., Garcia-del Portillo F., Garrido P.,			
RA	Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,			
RA	Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,			
RA	Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,			
RA	Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Puccell R.,			
RA	Rommel B., Rose M., Schluter T., Simoes N., Tierrez A.,			
RA	Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;			
RT	"Comparative genomics of <i>Listeria</i> species."			
RL	Science 294:849-852(2001).			

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CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S51.
CC -----
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CC -----
CC EMBL: AL591975; CAC98442.1; -
CC Listlist: LHM00363;
CC DR InterPro: IPR005320; Peptidase_S51.
CC DR Pfam: PF03575; Peptidase_S51; 1.
CC KW Hypothetical protein; Hydrolase; Serine protease; Complete proteome.
CC FT ACT_SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 160 160 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC SQ SEQUENCE 205 AA; 22776 MW; 95A24BA0910C47D6 CMC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 205;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 146 NYDA 149

RESULT 40
Y382.LISIN STANDARD; PRT; 209 AA.
AC 09256;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Probable peptidase Lhm0382 (EC 3.4.-.-).
GN LHM0382.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.
OX NCBI_TaxId=1642;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Chardot A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domnan E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kutaprat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Norstle G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RA "Comparative genomics of Listeria species.";
RT Science 294:849-852(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S51.
CC -----
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CC -----
CC EMBL: AL596164; CAC95615.1; -
CC Listlist: LHM00382;
CC DR InterPro: IPR005320; Peptidase_S51.
CC DR Pfam: PF03575; Peptidase_S51; 1.
CC KW Hypothetical protein; Hydrolase; Serine protease; Complete proteome.
CC FT ACT_SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).

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FT ACT_SITE 160 160 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 209 AA; 23226 MW; C575DC41F48143E2 CMC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 1; Length 209;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 146 NYDA 149

RESULT 41
UBL3.HUMAN STANDARD; PRT; 230 AA.
AC P13374;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L3 (EC 3.4.19.12) (UCH-
DE L3) (Ubiquitin thiolesterase L3).
GN UCHL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=90049185; PubMed=2530630;
RA Wilkinson K.D., Lee K., Deshpande S., Duerksen-Hughes P.,
RA Boss J.M., Pohl J.;
RT "The neuron-specific protein PGP 9.5 is a ubiquitin carboxyl-terminal
RT hydrolyase.";
RL Science 246:670-673(1989).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN 13
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=97377017; PubMed=9233788;
RA Johnston S.C., Larsen C.N., Cook W.J., Wilkinson K.D., Hill C.P.;
RT "Crystal structure of a deubiquitinating enzyme (human UCH-L3) at
RT 1.8-A resolution.";
RL EMBO J. 16:3787-3796(1997).
CC -1- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUITINATED PROTEINS.
CC THIS ENZYME IS A THIOLESTERASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DISEASE: A DEFECT OR ALTERATION IN THE EXPRESSION OF ENZYMES
CC CATALYZING THE REMOVAL OF UBIQUITIN FROM UBIQUITIN-PROTEINS
CC SUCH AS ALZHEIMER'S DISEASE, PARKINSON'S DISEASE, PROGRESSIVE
CC SUPRANUCLEAR PALSY, AND PICK'S AND KUF'S DISEASE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL: M30496; AAA36791.1; -
CC EMBL: BC018125; AAA18125.1; -
CC PIR: A40085; A40085.
CC PDB: 1UCH; 2A-JUN-98.
CC MEROPS: C12.003; -.

```

DR Genew; HGNC:12515; UCHL3.
 DR MIM; 603090; -.
 DR InterPro: IPR001578; UCH_1.
 DR Pfam: PF01088; Peptidase_C12; 1.
 DR PRINTS; PR00707; UBC7HYDRLASE.
 DR PROSITE; PS00140; UCH_1; 1.
 KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family;
 3D-structure.
 FT ACT_SITE 95 95
 FT ACT_SITE 169 169
 FT ACT_SITE 184 184
 FT DOMAIN 40 57
 FT DOMAIN 178 186
 FT SEQUENCE 230 AA; 26182 MW; 8ACACE6E1D86FD55 CRC64;
 SO
 Query Match 100.0%; Score 23; DB 1; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 Db 140 NYDA 143

RESULT 42
 UBL_MOUSE STANDARD; PRT: 230 AA.
 ID UBL_MOUSE
 AC Q9JKB1; Q9EQX7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ubiquitin carboxyl-terminal hydrolase isozyme L3 (EC 3.4.19.12) (UCH-L3) (Ubiquitin thiolesterase L3).
 GN UCHL3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=20180078; PubMed=10713173;
 RA Kirihara L.J., Semenova E., Levorse J.M., Tilghman S.M.;
 RT "Expression and functional analysis of Uch-L3 during mouse development.";
 RT Mol. Cell. Biol. 20:2498-2504(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver, and Kidney;
 RX MEDLINE=21240090; PubMed=11341770;
 RA Osawa Y., Wang Y.-L., Osaka H., Aoki S., Wada K.;
 RT "Cloning, expression, and mapping of a mouse gene, Uchl4, highly homologous to human and mouse Uchl3.";
 RT Biochem. Biophys. Res. Commun. 283:627-633(2001).
 RL
 CC -1- FUNCTIONING OF UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
 CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
 CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O = ubiquitin + a thiol.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in various tissues. Highest expression in brain, liver, heart, kidney and testis.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
 CC
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DR EMBL; AF247358; AAF64193.1; -.
 DR EMBL; AB033370; BAB20094.1; -.
 DR HSSP; P15374; 1UCH.
 DR MEROPS; C12.003; -.
 DR MGD; MGI:1353274; UCHL3.
 DR InterPro: IPR001578; UCH_1.
 DR Pfam: PF01088; Peptidase_C12; 1.
 DR PRINTS; PR00707; UBC7HYDRLASE.
 DR PROSITE; PS00140; UCH_1; 1.
 KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family;
 3D-structure.
 FT ACT_SITE 95 95
 FT ACT_SITE 169 169
 FT ACT_SITE 184 184
 FT ACT_SITE 40 57
 FT DOMAIN 178 186
 FT DOMAIN 205 207
 FT CONFLICT 178 186
 FT SEQUENCE 230 AA; 26151 MW; F147991F3E69AC3 CRC64;
 SO
 Query Match 100.0%; Score 23; DB 1; Length 230;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 Db 140 NYDA 143

RESULT 43
 HEX8_ADE40 STANDARD; PRT: 233 AA.
 ID HEX8_ADE40
 AC P11821;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Hexon-associated protein precursor (Protein VIII).
 GN PVIII.
 OS Human adenovirus type 40.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=28284;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dugan;
 RX MEDLINE=94087748; PubMed=8263936;
 RA Davidson A.J., Telford E.A., Watson M.S., McBride K., Mautner V.;
 RT "The DNA sequence of adenovirus type 40.";
 RT J. Mol. Biol. 234:1308-1316(1993).
 RN [2]
 RP SEQUENCE OF 1-47 FROM N.A.
 RX MEDLINE=88160034; PubMed=3279700;
 RA Vos H.L., der Lee F.M., Reemst A.M.C.B., van Loon A.E.,
 RA Sussenbach J.S.;
 RT "The genes encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41.";
 RT Virology 163:1-10(1988).
 RL
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EMBL; L19443; AAC13972.1; -.
 DR EMBL; M19316; AAA52198.1; -.
 DR InterPro: IPR000646; Adeno_PVIII.
 DR Pfam: PF01310; Adeno_PVIII; 1.
 KW Hexon-associated protein.
 FT PROPEP 1 111
 FT CHAIN 112 233
 FT SITE 111 112
 FT SEQUENCE 233 AA; 25327 MW; D135E37D3C6A6DE5C CRC64;
 SO
 HEXON-ASSOCIATED PROTEIN.
 CLEAVAGE (BY ADENOVIRUS PROTEASE).

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OW protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 : Search time 21.3333 Seconds
(without alignments)
38.634 Million cell updates/sec

Title: PAT943-5
Perfect score: 23
Sequence: 1 nyda 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	23	100.0	26	4	Q16782
2	23	100.0	36	2	Q93HR1
3	23	100.0	62	16	Q8ZMH4
4	23	100.0	63	3	Q96UY9
5	23	100.0	63	12	Q8V9U8
6	23	100.0	64	4	Q15423
7	23	100.0	65	5	Q26799
8	23	100.0	66	16	Q8R908
9	23	100.0	67	13	Q9PSM7
10	23	100.0	70	11	Q9QMA6
11	23	100.0	77	2	Q46529
12	23	100.0	80	5	Q9N7A7
13	23	100.0	80	11	Q63051
14	23	100.0	81	2	P72388
15	23	100.0	83	17	Q97BD6
16	23	100.0	85	16	Q97HX9

17	23	100.0	88	12	Q92350	human papill
18	23	100.0	88	12	Q92357	human papill
19	23	100.0	88	12	Q84218	human papill
20	23	100.0	89	3	Q96UY7	gelsinospo
21	23	100.0	92	2	Q9K365	streptococc
22	23	100.0	92	2	Q9LA7	streptococc
23	23	100.0	92	2	Q9LA6	streptococc
24	23	100.0	94	13	Q9PT87	gallus gall
25	23	100.0	97	2	Q9X3P9	streptococc
26	23	100.0	97	2	Q9X3Q0	streptococc
27	23	100.0	97	2	Q9X3Q1	streptococc
28	23	100.0	97	2	Q9WW51	streptococc
29	23	100.0	97	2	Q9WW50	streptococc
30	23	100.0	100	16	Q927D0	listeria in
31	23	100.0	106	16	Q83W8	listeria in
32	23	100.0	108	16	Q9PH17	listeria in
33	23	100.0	110	5	Q9X019	listeria in
34	23	100.0	111	6	Q9XSG7	caenorhabdi
35	23	100.0	112	12	P88807	felis silve
36	23	100.0	112	16	Q92B39	human papil
37	23	100.0	114	13	P79900	oncocythnu
38	23	100.0	120	2	Q8RL6	bradyrhizob
39	23	100.0	120	11	Q8RI22	mus muscicu
40	23	100.0	121	5	Q9V8Y8	drosophila
41	23	100.0	122	4	Q16834	homo sapien
42	23	100.0	122	4	Q16730	homo sapien
43	23	100.0	122	4	Q96GNO	homo sapien
44	23	100.0	122	5	Q96SP8	holothuria
45	23	100.0	122	6	Q29514	oryctolagus

ALIGNMENTS

RESULT 1
ID Q16782 PRELIMINARY; PRT; 26 AA.
AC Q16782;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Serum amyloid A protein (Fragment).
GN HUSALG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE-85252712; PubMed-3839415;
RX MEDLINE-85252712; PubMed-3839415;
RA Sipe J., Colten H., Goldberger G., Edge M.D., Tack B., Cohen A.,
Whitehead A.S.;
RT "Human serum amyloid A (SAA): biosynthesis and postsynthetic
processing of presAA and structural variants defined by complementary
DNA."
RT Biochemistry 24:2931-2936(1985).
RN [2]
RP MEDLINE-92022342; PubMed-1656519;
RX MEDLINE-92022342; PubMed-1656519;
RA Belts J.C., Edbrooke M.R., Thakker R.V., Woo P.;
RT "The human acute-phase serum amyloid A gene family: structure,
evolution and expression in hepatoma cells."
RT Scand. J. Immunol. 34:471-482(1991).
RN [3]
RP MEDLINE-93290347; PubMed-8512321;
RX MEDLINE-93290347; PubMed-8512321;
RA Baba S., Toshi T., Kasama T., Fujie M., Shirasawa H.;
RT "A novel polymorphism of human serum amyloid A protein. SAA1 gamma, is
characterized by alanines at residues 52 and 57."
RT Arch. Biochem. Biophys. 303:361-366(1993).
RN [4]
RP MEDLINE-93290347; PubMed-8512321;
RX MEDLINE-93290347; PubMed-8512321;
RA Baba S., Masago S., Shirasawa H., Tsutsui Y.;

RT "A novel allelic variant of human serum amyloid A, SAA1 gamma, is a
 RT probable risk factor for inflammation-related AA-amyloidosis."
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 CC COMPLEX (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
 DR EMBL: D32001; BAA06768.1; -.
 DR InterPro: IPR000096; Serum_amyloid_A.
 DR Pfam: PF00277; SAA_proteins; 1.
 DR PRODom: PD002112; Serum_amyloid_A; 1.
 DR PROSITE: PS00992; SAA; 1.
 DR Acute phase; Amyloid; HDL; Plasma.
 FT NON_TER 1 19 A -> V (IN REF. 1).
 FT VARIANT 24 24 A -> V (IN REF. 2).
 FT SEQUENCE 26 AA; 2834 MW; 20952938D5E5AB2D CRC64;

Query Match 100.0%; Score 23; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 8 NYDA 11

RESULT 2
 O93HRI PRELIMINARY; PRT; 36 AA.
 AC O93HRI;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Gyrase B (Fragment).
 GN GYRB.
 OS Thermus thermophilus.
 OC Bacteria; Thermus/Delnococcus group; Deinococci; Thermales;
 OC Thermaceae; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB27;
 RA Hosino T., Nonaka E., Kobayashi H., Kousge T.;
 RT "XhoI-type restriction and modification system exists in Thermus
 RT thermophilus HB27";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB065587; BAB68512.1; -.
 DR InterPro: IPR00910; HMG_12_box.
 DR Pfam: PF00505; HMG_box; 1.
 FT NON_TER 36 36
 FT SEQUENCE 36 AA; 3849 MW; E615D83AC95F4500 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 2 NYDA 5

RESULT 3
 O8ZMH4 PRELIMINARY; PRT; 62 AA.
 ID O8ZMH4;
 AC O8ZMH4;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Putative cytoplasmic protein.
 GN STM2906.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.

OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Lettelle P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2."
 RT Nature 413:852-856(2001).
 DR EMBL: AE008832; AAL21786.1; -.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 62 AA; 6991 MW; 66F6990F502F08BB CRC64;

Query Match 100.0%; Score 23; DB 16; Length 62;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 32 NYDA 35

RESULT 4
 O96UY9 PRELIMINARY; PRT; 63 AA.
 AC O96UY9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mating-type protein Mat a-1 (Fragment).
 GN MATa-1.
 OS *Gelasinospora calospora*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; *Gelasinospora*.
 OX NCBI_TaxID=165411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FGSC 958;
 RX MEDLINE=21453106; PubMed=11567551;
 RA Dettman J.R., Harbinski F.M., Taylor J.W.;
 RT "Ascospore morphology is a poor predictor of the phylogenetic
 RT relationships of *Neurospora* and *Gelasinospora*."
 RL Fungal Genet. Biol. 34:49-61(2001).
 DR EMBL: AF388942; AAL28010.1; -.
 DR InterPro: IPR00910; HMG_12_box.
 DR Pfam: PF00505; HMG_box; 1.
 FT NON_TER 63 63
 FT SEQUENCE 63 AA; 7809 MW; 7A1F23BCE0EF7C8F CRC64;

Query Match 100.0%; Score 23; DB 3; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 60 NYDA 63

RESULT 5
 O8V9U8 PRELIMINARY; PRT; 63 AA.
 ID O8V9U8;
 AC O8V9U8;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ORF1 (Fragment).
 OS SEN virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.


```
OX NCBI_TaxID-136966;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEN-H.
RX MEDLINE-21536993; PubMed-11679921.
RA Wilson L.E., Umemura T., Astemborski J., Ray S.C., Alter H.J.,
RT "Dynamics of SEN Virus Infection among Injection Drug Users.";
RL J. Infect. Dis. 184:1315-1319(2001).
DR EMBL: AY052821; AAL14827.1.
DR InterPro: IPR004219; TVTVirus_Unk.
DR Pfam: PF02956; TT_ORF1; 1.
FT NON_TER 1
SQ SEQUENCE 63 AA; 7374 MW; 8A8B3939FA402D3E CRC64;

Query Match 100.0%; Score 23; DB 12; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 37 NYDA 40

RESULT 6
ID 015423 PRELIMINARY: PRT; 64 AA.
AC 015423;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SAA protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE-90262544; PubMed-1971508;
RA Steinkasserer A., Weiss E.H., Schwaebel W., Linke R.P.;
RT "Heterogeneity in human serum amyloid A protein. Five different
RT variants from one individual demonstrated by cDNA sequence analysis.";
RL Blochem. J. 268:187-193(1990).
DR EMBL: X51443; CA35808.1.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR PRODom: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00197; SAA; 1.
FT NON_TER 1
SQ SEQUENCE 64 AA; 7079 MW; 057D6C9B0BE06238 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 52 NYDA 55

RESULT 7
ID 026799 PRELIMINARY: PRT; 65 AA.
AC 026799;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Protein kinase (Fragment).
OS Trypanosoma brucei.
```

```
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID-5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TRE0667;
RX MEDLINE-94171906; PubMed-8126084;
RA Hua S.B., Wang C.C.;
RT "Differential accumulation of a protein kinase homolog in Trypanosoma
RT brucei.";
RL J. Cell. Biochem. 54:20-31(1994).
DR EMBL: L10994; AAL19806.2.
DR InterPro: IPR00719; Euk_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRODom: PD000001; Euk_pkinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KM kinase.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7463 MW; A701F31B9D7BADAF CRC64;

Query Match 100.0%; Score 23; DB 5; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 54 NYDA 57

RESULT 8
ID 089908 PRELIMINARY: PRT; 66 AA.
AC 089908;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein TTE1824.
GN TTE1824.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID-119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WBAT / JCM11007;
RX MEDLINE-21992816; PubMed-11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013134; AAM25015.1.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 66 AA; 8172 MW; AF00402B3B8D9DA0 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
DB 23 NYDA 26

RESULT 9
ID 09PSM7 PRELIMINARY: PRT; 67 AA.
AC 09PSM7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AA=9 kDa reactive AA-type JOINT amyloid protein.
OS Gallus gallus (Chicken).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=96228953; PubMed=8633201;
 RX Landman W.J., Sletten K., Koch C.A., Toonen P.C., Gruys E.;
 RT "Chicken joint amyloid protein is of the AA-type. I. Characterization
 of the amyloid protein.";
 RL Scand. J. Immunol. 43:210-218(1996).
 DR InterPro: IPR000096; Serum_amyloid_A.
 DR Pfam: PF00277; SAA_proteins; 1.
 DR PRINTS: PR00306; SERUMAMYLID.
 DR PRODOM: PD002112; Serum_amyloid_A; 1.
 DR SMART: SM00197; SAA; 1.
 SQ SEQUENCE 67 AA; 7463 MW; 0D1DC87116ABA706 CRC64;

Query Match 100.0%; Score 23; DB 13; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2; 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 45 NYDA 48

RESULT 10
 09QWA6

ID 09QWA6 PRELIMINARY; PRT; 70 AA.

AC 09QWA6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Serum amyloid A protein (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus;
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=94126673; PubMed=8296166;
 RX Niewold T.A., Murphy C., Gruys E.;
 RL Scand. J. Immunol. 39:225-227(1994).
 CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 CC COMPLEX (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
 DR InterPro: IPR000096; Serum_amyloid_A.
 DR PRINTS: PR00306; SERUMAMYLID.
 DR PRODOM: PD002112; Serum_amyloid_A; 1.
 DR SMART: SM00197; SAA; 1.
 DR PROSITE: PS00992; SAA; 1.
 KW Acute phase; Amyloid; HDL; Plasma.
 FT NON_TER 1
 FT NON_CONS 22 23
 FT NON_TER 70
 SQ SEQUENCE 70 AA; 7897 MW; 568E516C9DA5E84C CRC64;

Query Match 100.0%; Score 23; DB 11; Length 70;
 Best Local Similarity 100.0%; Pred. No. 2; 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 29 NYDA 32

RESULT 11
 046529 PRELIMINARY; PRT; 77 AA.

AC 046529;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE ORFC protein (Fragment).
 OS Bacteroides nodosus (Dichelobacter nodosus).
 OC Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
 OC Dichelobacter.
 OX NCBI_TaxID=870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AI98;
 RX MEDLINE=97090407; PubMed=8936315;
 RA La Fontaine S., Kood J.L.;
 RT "Organization of ribosomal RNA genes from the footrot pathogen
 RT Dichelobacter nodosus.";
 RL Microbiology 142:889-899(1996).
 DR EMBL: U26682; AAC13873.1; -.
 DR HSSP: P00349; 2PGD.
 DR InterPro: IPR001744; 6PGD.
 DR Pfam: PF00393; 6PGD; 1.
 FT NON_TER 1
 SQ SEQUENCE 77 AA; 8431 MW; 668EBBA08B49B78 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 74 NYDA 77

RESULT 12
 09N7A7

ID 09N7A7 PRELIMINARY; PRT; 80 AA.

AC 09N7A7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Probable heat-shock protein (Fragment).
 GN LM28.327.
 OS Leishmania major.
 OC Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390935; CAC01030.1; -.
 DR InterPro: IPR001023; Hsp70.
 DR Pfam: PF00012; Hsp70; 1.
 DR PRODOM: PD000089; Hsp70; 1.
 FT NON_TER 1
 FT NON_CONS 80 80
 FT NON_TER 80
 SQ SEQUENCE 80 AA; 9183 MW; 6FADCCA0F94BA82A CRC64;

Query Match 100.0%; Score 23; DB 5; Length 80;
 Best Local Similarity 100.0%; Pred. No. 3; 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 ||||
 DB 9 NYDA 12

RESULT 13
 063051 PRELIMINARY; PRT; 80 AA.
 AC 063051;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Apolipoprotein B (Fragment).
GN APOB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=6908966; PubMed=2911593;
RA Tenyson G.E., Sabatos C.A., Higuchi K., Meglin N., Brewer H.B.Jr.,
RT Expression of apolipoprotein B mRNAs encoding higher- and lower-
RT molecular weight isoforms in rat liver and intestine."
RL Proc. Natl. Acad. Sci. U.S.A. 86:500-504(1989).
DR EMBL: M23049; AAA04753.1; -.
KW Lipoprotein.
FT NON_TER 1 1
SQ SEQUENCE 80 AA; 9485 MW; DB679A0C93AANA2F7 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 74 NYDA 77

RESULT 14
P72388 PRELIMINARY; PRT; 81 AA.
ID P72388
AC P72388;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Transposase (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON-TN551;
RA McNamara P.M., Iandolo J.J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U75367; AAB18959.1; -.
DR InterPro: IPR002513; Transposase_7.
DR Pfam: PF01526; Transposase_7; 1.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9490 MW; B957359583F72C12 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 39 NYDA 42

RESULT 15
Q97BD6 PRELIMINARY; PRT; 83 AA.
ID Q97BD6
AC Q97BD6;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein TV0520.
GN TV0520 OR TVG0510164.
OS Thermoplasma volcanium.

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OC Archaea; Euryarchaeota; Thermoplasmatata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GSSI / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H.,
RA Kawashima T., Matarabe K., Makino S.-I., Higuchi S.,
RA Nunoshida T., Yamamoto T., Aramaki H., Makino K., Kaneshiro K., Kawamoto T.,
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium."
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL: AP000992; BAB59662.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 83 AA; 9869 MW; BC587A016EBD7DAE CRC64;

Query Match 100.0%; Score 23; DB 17; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 25 NYDA 28

RESULT 16
Q97HX9 PRELIMINARY; PRT; 85 AA.
ID Q97HX9
AC Q97HX9;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Hypothetical CF-8 family protein CAC1877.
GN CAC1877.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusev R.L., Sabathe F., Doucetle-Stamm L., Soucaille P., Daly M.J.,
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007696; AAK79841.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 85 AA; 9954 MW; 6DBFE46C8A85900E CRC64;

Query Match 100.0%; Score 23; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 4 NYDA 7

RESULT 17
O92350 PRELIMINARY; PRT; 88 AA.
ID O92350
AC O92350;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE l1 protein (Fragment).
OS Human papillomavirus.
OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV22B;
RX MEDLINE=20295075; PubMed=10834958;
RA Berkhout R.J.M., Bouwes Bavinck J.N., ter Schegget J.;
RT "Persistence of Human Papillomavirus DNA in Benign and (Pre)malignant
RL Skin Lesions from Renal Transplant Recipients.";
RJ J. Clin. Microbiol. 38:2087-2096(2000).
DR EMBL; AF091439; AAC63347.1; -
RT InterPro: IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR Prodom; PD000544; PV_capsid_L1; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 88 AA; 10086 MW; E91F3B8BF7B5B1A6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 12; Length 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 11 NYDA 14

RESULT 18
092357 PRELIMINARY; PRT; 88 AA.
AC 092357;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE L1 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPVX10B;
RX MEDLINE=20295075; PubMed=10834958;
RA Berkhout R.J.M., Bouwes Bavinck J.N., ter Schegget J.;
RT "Persistence of Human Papillomavirus DNA in Benign and (Pre)malignant
RL Skin Lesions from Renal Transplant Recipients.";
RJ J. Clin. Microbiol. 38:2087-2096(2000).
DR EMBL; AF091446; AAC63354.1; -
RT InterPro: IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR Prodom; PD000544; PV_capsid_L1; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 88 AA; 10032 MW; 21A64076DC03298A CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 12; Length 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 11 NYDA 14

RESULT 19
084218 PRELIMINARY; PRT; 88 AA.
AC 084218;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE L1 (Fragment).
GN L1.

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OS Human papillomavirus type 22.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=37954;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KREMSDORF ET AL;
RX MEDLINE=95270695; PubMed=7751378;
RA Berkhout R.J., Tieben L.M., Smits H.L., Bavinck J.N., Vermeer B.J.,
RT ter Schegget J.;
RT "Nested PCR approach for detection and typing of epidermodysplasia
RT verruciformis-associated human papillomavirus types in cutaneous
RL cancers from renal transplant recipients.";
RJ J. Clin. Microbiol. 33:690-695(1995).
DR EMBL; L38912; AAA74306.1; -
RT InterPro: IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR Prodom; PD000544; PV_capsid_L1; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 88 AA; 10084 MW; FB14A8BE9AA5058 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 12; Length 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 11 NYDA 14

RESULT 20
096UY7 PRELIMINARY; PRT; 89 AA.
AC 096UY7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Matrig-type protein Mat a-1 (Fragment).
GN MATa-1.
OS Gelasinospora tetrasperma.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Gelasinospora.
OX NCBI_TaxID=94610;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGSC 7033;
RX MEDLINE=21453106; PubMed=11567551;
RA Dettman J.R., Harbinski F.M., Taylor J.W.;
RT "Ascospore morphology is a poor predictor of the phylogenetic
RT relationships of Neurospora and Gelasinospora.";
RJ Fungal Genet. Biol. 34:49-61(2001).
DR EMBL; AF388944; AAL28012.1; -
RT InterPro: IPR000910; HMG_box; 1.
DR Pfam; PF00505; HMG_box; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 89 AA; 10984 MW; 8DDDC4497AC9A29 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 3; Length 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
DB 86 NYDA 89

RESULT 21
09K365 PRELIMINARY; PRT; 92 AA.
AC 09K365;
DT 01-OCT-2000 (TREMBlrel. 15, Created)

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DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.
OS Streptococcus mitis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=28037;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-V8, AND V1;
RX MEDLINE-99437795; PubMed-10508036;
RA Ferrandiz M.J., Oteo J., Aracil B., Gomez-Garcas J.L.,
RA De La Campa A.G.;
RT "Drug efflux and parC mutations are involved in fluoroquinolone
resistance in viridans group streptococci.";
RL Antimicrob. Agents Chemother. 43:2520-2523(1999).
DR EMBL; AF144785; AAF67236.1; -.
DR EMBL; AF144784; AAF67235.1; -.
DR HSSP; P09097; IAB4.
DR InterPro: IPR002205; DNA_topoisolv.
DR Pfam; PF00521; DNA_topoisolv; 1.
DR ProDom; PD000742; DNA_topoisolv; 1.
DR SMART; SM00434; TOP4c; 1.
FT NON_TER 1 1
FT SEQUENCE 92 AA; 10497 MW; 37D040221C604AB6 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 83 NYDA 86

RESULT 22
O9LA7 PRELIMINARY; PRT; 92 AA.
AC O9LA7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.
OS Streptococcus oralis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-V9;
RX MEDLINE-99437795; PubMed-10508036;
RA Ferrandiz M.J., Oteo J., Aracil B., Gomez-Garcas J.L.,
RA De La Campa A.G.;
RT "Drug efflux and parC mutations are involved in fluoroquinolone
resistance in viridans group streptococci.";
RL Antimicrob. Agents Chemother. 43:2520-2523(1999).
DR EMBL; AF144786; AAF67237.1; -.
DR HSSP; P09097; IAB4.
DR InterPro: IPR002205; DNA_topoisolv.
DR Pfam; PF00521; DNA_topoisolv; 1.
DR ProDom; PD000742; DNA_topoisolv; 1.
DR SMART; SM00434; TOP4c; 1.
FT NON_TER 1 1
FT SEQUENCE 92 AA; 10479 MW; 679440221C604AB6 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 83 NYDA 86

RESULT 23
O9LA6 PRELIMINARY; PRT; 92 AA.
AC O9LA6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.
OS Streptococcus mitis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=28037;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-V10;
RX MEDLINE-99437795; PubMed-10508036;
RA Ferrandiz M.J., Oteo J., Aracil B., Gomez-Garcas J.L.,
RA De La Campa A.G.;
RT "Drug efflux and parC mutations are involved in fluoroquinolone
resistance in viridans group streptococci.";
RL Antimicrob. Agents Chemother. 43:2520-2523(1999).
DR EMBL; AF144787; AAF67238.1; -.
DR HSSP; P09097; IAB4.
DR InterPro: IPR002205; DNA_topoisolv.
DR Pfam; PF00521; DNA_topoisolv; 1.
DR ProDom; PD000742; DNA_topoisolv; 1.
DR SMART; SM00434; TOP4c; 1.
FT NON_TER 1 1
FT SEQUENCE 92 AA; 10467 MW; 05ED40220B477AA6 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 83 NYDA 86

RESULT 24
O9PT87 PRELIMINARY; PRT; 94 AA.
AC O9PT87;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Proteinkin convertase PC6 (Fragment).
GN PC6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE-20392157; PubMed-10933711;
RA Feldmann A., Schaefer M.R.H., Garten W., Klenk H.D.;
RT "Targeted infection of endothelial cells by the Avian influenza Virus
J. Virol. 74:8018-8027(2000).
DR EMBL; AJ252169; CAB65905.1; -.
DR HSSP; Q45670; IDB1.
DR MEROPS; S08.076; -.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.

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DR PROSITE: PS00137; SUBRTLASE_HIS; 1.
RT NON_TER 1
FT NON_TER 94
SQ SEQUENCE 94 AA; 10010 MW; AAEA8028D4E2AF61 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 13; Length 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   ||||
Db 5 NYDA 8

RESULT 25
Q9X3P9 PRELIMINARY; PRT; 97 AA.
AC Q9X3P9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.
OS Streptococcus oralis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1180;
RX MEDLINE=99013551; PubMed=9797205;
RA Gonzalez I., Georgiou M., Alcalde F., Balas D., Linares J.,
RA de la Campa A.G.;
RT "Fluoroquinolone resistance mutations in the parC, parE, and gyra
RT genes of clinical isolates of viridans group streptococci.";
RL Antimicrob. Agents Chemother. 42:2792-2798(1998).
DR EMBL: AF079200; AAD23327.1; -.
DR HSSP: P09097; 1AB4.
DR InterPro: IPR002205; DNA_topoisomIV.
DR Pfam: PF00521; DNA_topoisomIV; 1.
DR ProDom: PD000742; DNA_topoisomIV; 1.
DR SMART: SM00434; TOP4C; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 11192 MW; 275B405D7EE61E25 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   ||||
Db 88 NYDA 91

RESULT 26
Q9X300 PRELIMINARY; PRT; 97 AA.
AC Q9X300;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.
OS Streptococcus oralis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3870;
RX MEDLINE=99013551; PubMed=9797205;
RA Gonzalez I., Georgiou M., Alcalde F., Balas D., Linares J.,

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RA de la Campa A.G.;
RT "Fluoroquinolone resistance mutations in the parC, parE, and gyra
RT genes of clinical isolates of viridans group streptococci.";
RL Antimicrob. Agents Chemother. 42:2792-2798(1998).
DR EMBL: AF079201; AAD23328.1; -.
DR HSSP: P09097; 1AB4.
DR InterPro: IPR002205; DNA_topoisomIV.
DR Pfam: PF00521; DNA_topoisomIV; 1.
DR ProDom: PD000742; DNA_topoisomIV; 1.
DR SMART: SM00434; TOP4C; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 11176 MW; 275B58E6DD76A586 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   ||||
Db 88 NYDA 91

RESULT 27
Q9X301 PRELIMINARY; PRT; 97 AA.
AC Q9X301;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.
OS Streptococcus mitis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=28037;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=197;
RX MEDLINE=99013551; PubMed=9797205;
RA Gonzalez I., Georgiou M., Alcalde F., Balas D., Linares J.,
RA de la Campa A.G.;
RT "Fluoroquinolone resistance mutations in the parC, parE, and gyra
RT genes of clinical isolates of viridans group streptococci.";
RL Antimicrob. Agents Chemother. 42:2792-2798(1998).
DR EMBL: AF079205; AAD23332.1; -.
DR HSSP: P09097; 1AB4.
DR InterPro: IPR002205; DNA_topoisomIV.
DR Pfam: PF00521; DNA_topoisomIV; 1.
DR ProDom: PD000742; DNA_topoisomIV; 1.
DR SMART: SM00434; TOP4C; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 11115 MW; 661A4CA6DC66B380 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
   ||||
Db 88 NYDA 91

RESULT 28
Q9MW51 PRELIMINARY; PRT; 97 AA.
AC Q9MW51;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.

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OS Streptococcus mltis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=28037;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=888, NCTC 12261, 14, 112, 718, AND 720;
RA Gonzalez I., Georgiou M., Alcalde F., Balas D., Linares J.,
  de la Campa A.G.;
RT "Fluoroquinolone resistance mutations in the parC, parE and gyrA genes
  of clinical isolates of viridans group Streptococci.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079208; AAD33335.1; -
DR EMBL; AF079202; AAD33328.1; -
DR EMBL; AF079203; AAD33330.1; -
DR EMBL; AF079204; AAD33331.1; -
DR EMBL; AF079206; AAD33333.1; -
DR EMBL; AF079207; AAD33334.1; -
DR HSSP; P09097; IAB4.
DR InterPro; IPR002205; DNA_topoisomIV.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR ProDom; PD000742; DNA_topoisomIV; 1.
DR SMART; SM00434; Topac; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 11115 MW; 275848F7DC66B487 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 88 NYDA 91

RESULT 29
O9MW50 PRELIMINARY; PRT; 97 AA.
AC O9MW50;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE DNA gyrase subunit A (Fragment).
GN GYRA.
OS Streptococcus oralis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10557, AND NCTC 11427;
RA Gonzalez I., Georgiou M., Alcalde F., Balas D., Linares J.,
  de la Campa A.G.;
RT "Fluoroquinolone resistance mutations in the parC, parE and gyrA genes
  of clinical isolates of viridans group Streptococci.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079199; AAD33326.1; -
DR EMBL; AF079198; AAD33325.1; -
DR HSSP; P09097; IAB4.
DR InterPro; IPR002205; DNA_topoisomIV.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR ProDom; PD000742; DNA_topoisomIV; 1.
DR SMART; SM00434; Topac; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 11115 MW; 275848F7DC66B487 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 88 NYDA 91

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Db 88 NYDA 91

RESULT 30
O927D0 PRELIMINARY; PRT; 100 AA.
AC O927D0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Hypothetical protein lin2859.
GN LIN2859.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacilliales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
  Baquero F., Berche P., Bioecker H., Brandt P., Chakraborty T.,
  Chardit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
  Domann E., Dominguez-Bernal G., Duchaud E., Durrant L., Dussurget O.,
  Entlan K.-D., Fsihi H., Garcia-Lopez N., Hain T., Haut J., Jackson D.,
  Gautier L., Goebel W., Gomez-Iopez N., Hain T., Haut J., Jackson D.,
  Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
  Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
  Nordstiel G., Novella S., de Pablos B., Perez-Diaz J.-C., Pucell R.,
  Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
  Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596173; CAC98085.1; -
DR Listlist; LIN02859; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 100 AA; 11061 MW; 283AB6995C3E2P6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 16; Length 100;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYDA 4
Db 31 NYDA 34

RESULT 31
O8Y3W8 PRELIMINARY; PRT; 106 AA.
AC O8Y3W8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Hypothetical protein lmo2711.
GN LMO2711.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacilliales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-E / SEROVAR 1/2A;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
  Baquero F., Berche P., Bioecker H., Brandt P., Chakraborty T.,
  Chardit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
  Domann E., Dominguez-Bernal G., Duchaud E., Durrant L., Dussurget O.,
  Entlan K.-D., Fsihi H., Garcia-Lopez N., Hain T., Haut J., Jackson D.,
  Gautier L., Goebel W., Gomez-Iopez N., Hain T., Haut J., Jackson D.,
  Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
  Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

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RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
 RT "Comparative genomics of *Listeria species.*";
 RT Science 294:849-852(2001).
 DR EMBL: AL591984; CAD00924.1; -.
 DR Listlist; LMO02711; -.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 106 AA; 11714 MW; 40175118A239A833 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 106;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 Db 31 NYDA 34

RESULT 32

O9PH17 PRELIMINARY; PRT; 108 AA.
 AC O9PH17;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein Xfa0018.
 GN Xfa0018.
 OS *Xylella fastidiosa.*
 OC Plasmid pXP51.
 CC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 NC NCB1_TaxID=23711;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;

RA Simpson A.J.G., Keinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.P., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
 RA Colaço N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteleiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Pelxoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quagga R.B., Roberto P.G., Rodrigues V.V., de Rosa A.J.M.,
 RA da Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA de Souza J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa.*";
 RL Nature 406:151-159(2000).
 DR EMBL: AE003851; AAF85587.1; -.
 DR InterPro: IPR000897; SRP54.
 DR PROSITE: PS00300; SRP54; UNKNOWN.1.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 108 AA; 12462 MW; 2F9ABCI76A1DDE1B CRC64;

Query Match 100.0%; Score 23; DB 16; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NYDA 4
 Db 76 NYDA 79

RESULT 33

O9XU19 PRELIMINARY; PRT; 110 AA.
 AC O9XU19;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ZC334.1 protein.
 GN ZC334.1.
 OS *Caenorhabditis elegans.*
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCB1_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McJury K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C. elegans*: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z82082; CAB04962.1; -.
 SO SEQUENCE 110 AA; 12423 MW; 1F52C1593A7EALF0 CRC64;

Query Match 100.0%; Score 23; DB 5; Length 110;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
 Db 79 NYDA 82

RESULT 34

O9XSG7 PRELIMINARY; PRT; 111 AA.
 AC O9XSG7;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Serum amyloid A protein (Fragment).
 GN SAA.
 OS *Felis silvestris catus* (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OC NCB1_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Ohno K., Terado M., Iwata H., Inokuma H., Onishi T.;
 RT "Expression of recombinant feline serum amyloid A (SAA) protein.";
 RL J. Vet. Med. Sci. 0:0-0(1999).
 CC CC
 CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 CC COMPLEX (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
 DR EMBL: AF136718; AAD24489.1; -.
 DR InterPro: IPR000096; Serum_amyloid_A.
 DR Pfam: PF00277; SAA_proteins; 1.
 DR PRINTS: PR00306; SERUMAMYL0ID.
 DR ProDom: PD002112; Serum_amyloid_A; 1.
 DR SMART: SM00197; SAA; 1.
 DR PROSITE: PS00992; SAA; 1.

KW Acute phase; Amyloid; HDL; Plasma.
 FT NON_TER 1
 SQ SEQUENCE 111 AA; 12547 MW; D9392BD358AF5D22 CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 6; Length 111;
 RT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
 DE Major capsid protein LI (Fragment).
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RTX10;
 RT "Human papillomavirus DNA in non-melanoma skin cancers of a renal transplant recipient."
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; u85663; AAB61648.1; -.
 DR InterPro: IPR002210; PV_capsid_L1.
 DR Pfam: PF00500; late_protein_L1; 1.
 DR ProDom: PD000544; PV_capsid_L1; 1.
 FT NON_TER 1
 FT SEQUENCE 112 AA; 12730 MW; FF5F93248BA3C01 CRC64;
 SQ
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 12; Length 112;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NYDA 4
 DB 21 NYDA 24

RESULT 36
 092B39 PRELIMINARY; PRT; 112 AA.
 AC 092B39;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Hypothetical protein lin1712.
 GN LIN1712.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / SEROVAR 6A;
 RC PubMed-11679669;
 RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Denoux P.,
 RA Dommann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Medjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Tiaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlieter T., Simoes N., Thieret A.,
 RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.,
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
 DR EMBL; AL596169; CAC96943.1; -.
 DR L1stL1st, LIN01712; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 112 AA; 12344 MW; C63273F88BF9450C CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 16; Length 112;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NYDA 4
 DB 29 NYDA 32

RESULT 37
 092B39 PRELIMINARY; PRT; 114 AA.
 AC 092B39;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE Serum amyloid A protein precursor (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proteocephali; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=97131713; PubMed=8977214;
 RA Jensen L.E., Hiney M.P., Shields D.C., Uhlar C.M., Lindsey A.J.,
 RA Whitehead A.S.;
 RT "Acute phase proteins in Salmonids. Evolutionary analyses and acute phase response."
 RL J. Immunol. 158:384-392(1997).
 CC - FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL COMPLEX (BY SIMILARITY).
 CC - TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY SIMILARITY).
 CC - SIMILARITY: BELONGS TO THE SAA FAMILY.
 DR EMBL; X9387; CAA67766.1; -.
 DR InterPro: IPR000096; Serum_amyloid_A.
 DR Pfam: PF00277; SAA_proteins; 1.
 DR PRINTS; PR00306; SERUMAMYLID.
 DR ProDom: PD002112; Serum_amyloid_A; 1.
 DR SMART; SM00197; SAA; 1.
 DR PROSITE; PS00992; SAA; 1.
 KW Acute phase; Amyloid; HDL; Plasma; Signal.
 FT NON_TER 1
 FT SIGNAL <1 11
 FT CHAIN 12 114
 FT SEQUENCE 114 AA; 12693 MW; 02D96C6F2ABE232C CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 23; DB 13; Length 114;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NYDA 4
 DB 51 NYDA 54

RESULT 38
 08RLF6 PRELIMINARY; PRT; 120 AA.
 ID 08RLF6
 AC 08RLF6;

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DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Vira-like protein (Fragment).
GN VIRA.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USD1105PC4;
RA Mueller P.;
RT "A TrkP2 insertion in a virg-like transcriptional regulator of
RT Bradyrhizobium japonicum results in the formation of poorly infected
RT soybean nodules."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY081839; AAM12360.1; -.
FT NON-TER
SQ SEQUENCE 120 AA; 13449 MW; F71F579B698A94A7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 120;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 63 NYDA 66

RESULT 39
OBR122 PRELIMINARY; PRT; 120 AA.
AC OBR122;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Hypothetical 13.1 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022724; AAH22724.1; -.
KW Hypothetical protein.
FT NON-TER
SQ SEQUENCE 120 AA; 13077 MW; CD72B2A353596525 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 11; Length 120;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 20 NYDA 23

RESULT 40
O9V8Y8 PRELIMINARY; PRT; 121 AA.
AC O9V8Y8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG13873 protein.
GN CG13873
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC
```

```
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moadary C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weisskock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003794; AAF57516.1; -.
DR FlyBase; FBgn0034474; CG13873.
DR InterPro; IPR000746; PBP_GOBP_family.
DR Pfam; PF01395; PBP_GOBP; 1.
SQ SEQUENCE 121 AA; 13128 MW; 97AE86E03523AE9C CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 5; Length 121;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 4 NYDA 7

RESULT 41
O16834 PRELIMINARY; PRT; 122 AA.
ID O16834;
AC O16834;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Serum amyloid A protein precursor.
DE SAAB1 BETA.
GN SAAB1 BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```

RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=92022342; PubMed=1656519;
RA Betts J.C., Edbrooke M.R., Thakker R.V., Woo P.;
RT "The human acute-phase serum amyloid A gene family: structure,
evolution and expression in hepatoma cells.";
RL Scand. J. Immunol. 34:471-482(1991).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
COMPLEX (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
SIMILARITY).
CC AC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; X56652; CAA39974.1; -.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; Amyloid; HDL; Plasma; Signal.
FT SIGNAL
FT CHAIN 1 18 POTENTIAL.
FT SEQUENCE 122 AA; 13533 MW; D913BF06AA4107A2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 4; Length 122;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 59 NYDA 62

RESULT 42
OY 016730 PRELIMINARY; PRT; 122 AA.
AC 016730;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Serum amyloid A protein precursor.
GN SAA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=89034862; PubMed=3183061;
RA Kluge-Beckerman B., Dwulet F.E., Benson M.D.;
RT "Human serum amyloid A. Three hepatic mRNAs and the corresponding
proteins in one person.";
RL J. Clin. Invest. 82:1670-1675(1988).
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
COMPLEX (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
SIMILARITY).
CC AC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; M23700; AAA64801.1; -.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; Amyloid; HDL; Plasma; Signal.
FT SIGNAL
FT CHAIN 1 18 POTENTIAL.
FT SEQUENCE 122 AA; 13527 MW; C4AAB684EDCDB8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 4; Length 122;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 59 NYDA 62

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 59 NYDA 62

RESULT 43
OY 096QNO PRELIMINARY; PRT; 122 AA.
AC 096QNO;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Serum amyloid A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007022; AA07022.1; -.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR PROSITE; PS00992; SAA; UNKNOWN1.
SQ SEQUENCE 122 AA; 13533 MW; 43A57D56B371DC13 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 4; Length 122;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
Db 59 NYDA 62

RESULT 44
OY 09GSP8 PRELIMINARY; PRT; 122 AA.
AC 09GSP8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Serum amyloid A protein.
OS Holothuria glaberrima.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Holothuroidea; Aspidochirothacea; Aspidochirothida; Holothuriidae;
OC Holothuria.
OX NCB1_TaxID=31192;
RN [1]
RP SEQUENCE FROM N.A.
RA Santiago-Cardona P.G., Roig-Lopez J.L., Santiago C.L.,
RA Garcia-Arriaras J.E.;
RT "Holothuroid serum amyloid A protein.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
COMPLEX (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
SIMILARITY).
CC AC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; AF300706; AAG24633.1; -.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; Amyloid; HDL; Plasma.
FT SIGNAL
FT CHAIN 1 18 POTENTIAL.
FT SEQUENCE 122 AA; 13580 MW; 740FCE6C8661FDB8 CRC64;

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Query Match 100.0%; Score 23; DB 5; Length 122;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYDA 4
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 Db 58 NYDA 61

RESULT 45

Q29514 PRELIMINARY; PRT; 122 AA.
 ID Q29514;
 AC Q29514;
 DT 01-NOV-1996 (TREMBLREL. 01, Created)
 DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE Putative serum amyloid A protein.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91315474; PubMed=1859410;
 RA Ray B.K., Ray A.;
 RT "Molecular cloning and nucleotide sequence of complementary DNA
 encoding rabbit alpha 1-acid glycoprotein.";
 RL Biochem. Biophys. Res. Commun. 178:507-513(1991).
 CC -! FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
 CC COMPLEX (BY SIMILARITY).
 CC -! TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
 CC SIMILARITY).
 CC -! SIMILARITY: BELONGS TO THE SAA FAMILY.
 CC EMBL: X58728; CAA41560.1; -;
 DR InterPro: IPR000096; Serum_amyloid_A.
 DR Pfam: PF00277; SAA_proteins; 1.
 DR PRINTS: PR00306; SERUMAMYLID.
 DR ProDom: PD002112; Serum_amyloid_A; 1.
 DR SMART: SM00197; SAA; 1.
 DR PROSITE: PS00992; SAA; 1.
 KW Acute phase; Amyloid; HDL; Hypothetical protein; Plasma.
 SQ SEQUENCE 122 AA; 13509 MW; B635BER22907945 CRC64;

Query Match 100.0%; Score 23; DB 6; Length 122;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NYDA 4
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 Db 59 NYDA 62

Search completed: February 6, 2003, 11:22:02
 Job time : 23.333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 27.8333 Seconds
(without alignments)
19.150 Million cell updates/sec

Title: PAT943-6
Perfect score: 20
Sequence: 1 nlda 4

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 1695

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	4	22	AAE06901 Human amyloid prec
2	20	100.0	4	22	AAU06630 Asp2 recognition s
3	20	100.0	4	22	AAU07229 Human beta-amyloid
4	20	100.0	4	23	ABB06547 Beta-secretase rel
5	20	100.0	5	17	AAW00415 Interleukin-6 anta
6	20	100.0	5	18	AAW08217 Swedish double mut
7	20	100.0	5	19	AAW61151 APP Swedish double
8	20	100.0	5	20	AAI33751 Swedish mutant bet
9	20	100.0	5	22	AAW47261 Swedish mutation A
10	20	100.0	6	23	AAU78500 Beta secretase cle

11	20	100.0	8	21	AAV94771 Beta-secretase sub
12	20	100.0	8	22 <td>AAE10661 Human aspartyl pro</td>	AAE10661 Human aspartyl pro
13	20	100.0	8	22 <td>AAE02613 Human aspartyl pro</td>	AAE02613 Human aspartyl pro
14	20	100.0	8	23 <td>ABR78622 Human beta secreta</td>	ABR78622 Human beta secreta
15	20	100.0	9	19 <td>AAW62081 Fluorogenic protea</td>	AAW62081 Fluorogenic protea
16	20	100.0	9	21 <td>AAW07874 A peptide fragment</td>	AAW07874 A peptide fragment
17	20	100.0	9	21 <td>AAW07894 Substrate for beta</td>	AAW07894 Substrate for beta
18	20	100.0	9	22 <td>AAW32297 Protease indicator</td>	AAW32297 Protease indicator
19	20	100.0	9	23 <td>ABW09003 Peptide #1 used as</td>	ABW09003 Peptide #1 used as
20	20	100.0	9	23 <td>ABW06519 Beta-secretase rel</td>	ABW06519 Beta-secretase rel
21	20	100.0	9	23 <td>AAW50897 Oligopeptide subst</td>	AAW50897 Oligopeptide subst
22	20	100.0	9	23 <td>ABW07598 Synthetic oligopep</td>	ABW07598 Synthetic oligopep
23	20	100.0	9	23 <td>AAE16663 Oligopeptide subst</td>	AAE16663 Oligopeptide subst
24	20	100.0	9	23 <td>AAU74837 Synthetic amyloid</td>	AAU74837 Synthetic amyloid
25	20	100.0	10	18 <td>AAW08362 Beta-secretase sub</td>	AAW08362 Beta-secretase sub
26	20	100.0	10	20 <td>AAI33756 Synthetic oligopep</td>	AAI33756 Synthetic oligopep
27	20	100.0	10	21 <td>AAV59707 Beta-APP alpha-sec</td>	AAV59707 Beta-APP alpha-sec
28	20	100.0	10	22 <td>AAE10653 Human APP-Sw beta-</td>	AAE10653 Human APP-Sw beta-
29	20	100.0	10	22 <td>AAE06898 Human amyloid prec</td>	AAE06898 Human amyloid prec
30	20	100.0	10	22 <td>AAU06627 Synthetic Asp2 rec</td>	AAU06627 Synthetic Asp2 rec
31	20	100.0	10	22 <td>AAU07226 Human beta-amyloid</td>	AAU07226 Human beta-amyloid
32	20	100.0	10	22 <td>AAE02605 Human APP-Sw beta-</td>	AAE02605 Human APP-Sw beta-
33	20	100.0	10	22 <td>AAW47266 Peptide 5-5'/SW, fo</td>	AAW47266 Peptide 5-5'/SW, fo
34	20	100.0	10	22 <td>AAW66575 Synthetic peptide</td>	AAW66575 Synthetic peptide
35	20	100.0	10	22 <td>AAW61337 Swedish mutation p</td>	AAW61337 Swedish mutation p
36	20	100.0	10	23 <td>AAU99491 Peptide #2 used as</td>	AAU99491 Peptide #2 used as
37	20	100.0	10	23 <td>ABW78614 Beta-secretase spe</td>	ABW78614 Beta-secretase spe
38	20	100.0	10	23 <td>ABW06425 Human APP Swedish</td>	ABW06425 Human APP Swedish
39	20	100.0	11	22 <td>AAW51442 APP Swedish varian</td>	AAW51442 APP Swedish varian
40	20	100.0	11	22 <td>AAW5145 Asp 1 substrate se</td>	AAW5145 Asp 1 substrate se
41	20	100.0	11	22 <td>AAW97469 Beta-secretase swe</td>	AAW97469 Beta-secretase swe
42	20	100.0	11	23 <td>AAW52699 Amyloid precursor</td>	AAW52699 Amyloid precursor
43	20	100.0	12	23 <td>ABW08996 Biotinylated synth</td>	ABW08996 Biotinylated synth
44	20	100.0	12	23 <td>ABW07591 APP substrate pept</td>	ABW07591 APP substrate pept
45	20	100.0	12	23 <td>AAE16656</td>	AAE16656

ALIGNMENTS

RESULT 1	AAE06901 standard; peptide: 4 AA.
AAE06901	
XX	
AC	AAE06901;
XX	
DT	23-OCT-2001 (first entry)
XX	
DE	Human amyloid precursor protein (APP-Sw) beta-secretase peptide #2.
XX	
KW	Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein;
KW	beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW	neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
KW	neuroprotective; antisense therapy; APP-Sw; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200150829-A2.
XX	
PD	19-JUL-2001.
XX	
PF	09-MAY-2001; 2001WO-IB00799.
XX	
PR	09-MAY-2001; 2001WO-IB00799.
XX	
PA	(BIEN/) BIENKOWSKI M J.
PA	(GURN/) GURNEY M E.
PA	(HEIN/) HEINRIKSON R L.
PA	(PARO/) PARODI L A.
PA	(YANR/) YAN R.
XX	
PI	Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX	

DR WPI: 2001-483072/52.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PS Claim 129; Page 101; 185pp; English.
XX
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma-secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human amyloid precursor protein (APP-SW)
CC beta-secretase peptide related to the invention.
CC
SQ Sequence 4 AA:

Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
Db 1 NLDA 4

RESULT 2
AAU06630
ID AAU06630 standard; Peptide: 4 AA.
AC
XX AAU06630;
AC
XX 24-OCT-2001 (first entry)
DT
XX
DE Asp2 recognition site from APP-SW.
XX
KW Aspartyl protease; Asp2; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; APP-SW.
XX
OS Homo sapiens.
XX
XX WO200149098-A2.
PN
XX
PD 12-JUL-2001.
PD
XX
PE 09-MAY-2001; 2001WO-IB00798.
PE
XX
PR 09-MAY-2001; 2001WO-IB00798.
PR
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
XX
PI Blenkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
DR WPI: 2001-502549/55.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl

PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PS Claim 129; Page 101; 185pp; English.
XX
XX The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp2) protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-SW-beta-secretase peptide sequence (NLDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridize to
CC APP oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is the APP
CC beta-secretase peptide sequence from APP-SW, the Swedish mutation.
CC
SQ Sequence 4 AA:

Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
Db 1 NLDA 4

RESULT 3
AAU07229
ID AAU07229 standard; Peptide: 4 AA.
AC
XX AAU07229;
AC
XX 24-OCT-2001 (first entry)
DT
XX
DE Human beta-amyloid protein precursor, APP-beta secretase site peptide #2.
XX
XX Human: aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP-beta.
XX
OS Homo sapiens.
XX
XX WO200149097-A2.
PN
XX
PD 12-JUL-2001.
PD
XX
PE 09-MAY-2001; 2001WO-IB00797.
PE
XX
PR 09-MAY-2001; 2001WO-IB00797.
PR
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
XX
PI Blenkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

XX WPI; 2001-502548/55.

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity

PS Claim 129; Page 101; 185pp; English.

XX The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognizable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP-beta
 CC secretase site peptide substrate #2 used in assays of human Asp2 beta-
 CC secretase activity.

SO Sequence 4 AA;

Query Match 100.0%; Score 20; DB 22; Length 4;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
 ||||
 Db 1 NLDA 4

RESULT 4
 ABB06547

ID ABB06547 standard; Peptide; 4 AA.

XX ABB06547;

DT 31-MAY-2002 (first entry)

DE Beta-secretase related peptide SEQ ID NO:142.

XX Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KM aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
 KM Alzheimer's disease.

OS Homo sapiens.
 OS Synthetic.

PN WO200206306-A2.

PD 24-JAN-2002.

PF 19-JUL-2001; 2001WO-US23035.

PR 19-JUL-2000; 2000US-219795P.
 PR 12-MAR-2001; 2001US-275251P.

PA (PHAA) PHARMACIA & UPJOHN CO.

PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrikson RL;

DR WPI; 2002-216995/27.

XX Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease

PS Disclosure; Page 169; 186pp; English.

XX The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterized by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.

SO Sequence 4 AA;

Query Match 100.0%; Score 20; DB 23; Length 4;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
 ||||
 Db 1 NLDA 4

RESULT 5
 AAM00415

ID AAM00415 standard; peptide; 5 AA.

XX AAM00415;

DT 29-AUG-1996 (first entry)

DE Interleukin-6 antagonist peptide.

KW IL-6; antagonist; autoimmune disease.

OS Synthetic.

PN JP07324097-A.

PD 12-DEC-1995.

PF 30-MAY-1994; 94JP-0117259.

PR 30-MAY-1994; 94JP-0117259.

PA (DAIL) DAICEL CHEM IND LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.

DR WPI: 1996-065476/07.

XX Interleukin 6 antagonist - useful for treating autoimmune diseases
 PT Claims 3, 6; Pages 2, 3; 19pp; Japanese.

XX New IL-6 antagonists are provided which are of formula X-W-Y, in
 CC which X is H or an amino-protecting group, Y is OH or a carboxy-
 CC protecting group, and W is a peptide containing all or part of the
 CC sequence as given in AAM00401, AAM00402, AAM00403 or AAM00404, where any
 CC free mercapto groups in the sequence are optionally protected. The

CC Present sequence is a specifically preferred partial sequence of AAM00402
CC and is itself claimed as a new chemical entity.
CC The IL-6 antagonists are useful for treating autoimmune diseases.
XX

SO Sequence 5 AA;

Query Match 100.0%; Score 20; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
AC 2 NLDA 5

RESULT 6

ID AAM08217 standard; peptide; 5 AA.

XX AAM08217;

DT 05-SEP-1997 (first entry)

XX Swedish double mutant APP beta-cleavage site.

DE Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.

XX Homo sapiens.

XX MO9640885-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09985.

XX 07-JUN-1995; 95US-0485152.

XX 07-JUN-1995; 95US-0480498.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
PI Mcconlogue IC, Sinha S, Tan H;

DR WPI: 1997-052304/05.

PT Beta-secretase which specifically cleaves beta-amyloid precursor
PT protein; useful to screen for inhibitors useful in treatment of
PT Alzheimer's disease

XX Claim 5; Page 60; 92pp; English.

CC AAM08216, AAM08217 and AAM08350 represent beta-cleavage sites from
CC beta-amyloid precursor proteins (APP). These sequences are recognised by
CC the enzyme of the invention. The enzyme of the invention is
CC beta-secretase, and specifically cleaves beta-APP at one of these sites.
CC Normal processing of beta-APP is thought to occur via cleavage between
CC residues 16 and 17 of the beta-amyloid peptide region by an
CC alpha-secretase. Pathogenic processing is thought to occur by
CC beta-secretase cleavage of beta-APP. beta-secretase activity can be
CC detected and measured using a method of the invention, which detects at
CC least one of the beta-secretase cleavage products formed on cleavage. The
CC method can be used to determine whether a test substance inhibits
CC proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective
CC to at least partially inhibit beta-secretase activity can be used to
CC inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and
CC purification of beta-secretase will permit chemical modelling of a
CC critical event in the pathology of Alzheimer's disease.

XX Sequence 5 AA;

Query Match 100.0%; Score 20; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
DB 2 NLDA 5

RESULT 7
ID AAM61151 standard; peptide; 5 AA.

XX AAM61151;

XX 26-OCT-1998 (first entry)

XX APP Swedish double mutation cleavage site.

DE Beta-secretase; human; beta-amyloid precursor protein; APP;
KW protease; inhibitor; screening; Alzheimer's disease; therapy.

XX Homo sapiens.

XX WO9826059-A1.

XX 18-JUN-1998.

XX 11-DEC-1996; 96WO-US19549.

XX 11-DEC-1996; 96WO-US19549.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

PI Anderson JP, Chrysler SMS, Keim PS, Sinha S;

PI WPI: 1998-348519/30.

PT Novel beta-secretase which cleaves beta-amyloid precursor protein -
PT useful for screening for compounds which inhibit the cleavage and
PT are useful for treating Alzheimer's disease

XX Disclosure; Page 20; 39pp; English.

CC This peptide comprises the site of the 'Swedish' double mutation
CC beta-amyloid precursor protein (APP) (MP-C125 SW) that is cleaved
CC by a novel beta-secretase isolated from human 293 cells. This
CC protease cleaves APP at the N-terminus of the beta-amyloid peptide
CC (beta-AP) and is believed to be the putative beta-secretase
CC responsible for the pathogenic processing of APP to beta-AP in
CC Alzheimer's disease. Down's syndrome and HCHWA-D. Recombinant
CC fusion proteins (see AAM61152) were generated comprising the last
CC 125 amino acids of APP (wild-type (see AAM61150) or Swedish double
CC mutation) fused to the C-terminal end of maltose binding protein.
CC The fusion proteins were expressed in Escherichia coli, and used as
CC substrates for beta-secretase in beta-secretase inhibitor assays.
CC Compounds that inhibit APP cleavage by beta-secretase may be useful
CC in the treatment of Alzheimer's disease.

XX Sequence 5 AA;

Query Match 100.0%; Score 20; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
DB 2 NLDA 5

RESULT 8

ID AAY33751 standard; Protein; 5 AA.

XX AAY33751;

XX	09-NOV-1999	(first entry)	
DT			
XX	Swedish mutant beta-amyloid protein precursor (APP) cleavage site.		
DE			
XX	Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;		
KW	Alzheimer's disease; cleavage site; mutant.		
XX			
XX	Homo sapiens.		
OS	Synthetic.		
XX			
PN	US5942400-A.		
XX			
PD	24-AUG-1999.		
XX			
PF	07-JUN-1996;	96US-0659984.	
XX			
PR	07-JUN-1996;	96US-0659984.	
XX			
PR	07-JUN-1995;	95US-0480498.	
XX			
PR	07-JUN-1995;	95US-0485152.	
XX			
PA	(ELAN-) ELAN PHARM INC.		
XX			
PI	Anderson JP, Jacobson-Croak KL, Sinha S;		
XX			
DR	WPI: 1999-517417/43.		
XX			
PT	A method for detecting human beta-secretase cleavage of polypeptides		
XX	useful for identifying beta-secretase inhibitors		
PS			
PS	Examples; Column 28; 43pp; English.		
XX			
CC	This sequence is the Swedish mutant beta-amyloid protein precursor (APP)		
CC	cleavage site. APP is cleaved by beta-secretase AAY33741. The wild type		
CC	cleavage site AAY33750 and the Swedish mutant version are used in a		
CC	method for detecting human beta-secretase cleavage of polypeptides and		
CC	for identifying beta-secretase inhibitors. Inhibition of beta-secretase		
CC	activity would be useful for chemical modelling of a critical event in		
CC	the pathology of Alzheimer's disease. Inhibitors of beta-secretase would		
CC	be useful for the prevention and treatment of Alzheimer's disease and		
XX	Down's Syndrome.		
XX			
SO	Sequence	5 AA;	
XX			
Query Match	100.0%;	Score 20;	DB 20;
Best Local Similarity	100.0%;	Pred. No. 7.8e+05;	Length 5;
Matches	4;	Conservative	0;
		Mismatches	0;
		Indels	0;
		Gaps	0;
Oy	1 NLDA 4		
Db	2 NLDA 5		
XX			
RESULT 9			
AAB47261			
ID	AAB47261 standard; Peptide: 5 AA.		
XX			
AC	AAB47261;		
XX			
DT	18-JUN-2001 (first entry)		
XX			
DE	Swedish mutation APP sequence for cleavage by beta-secretase.		
XX			
KW	Beta-secretase; Isotype; beta-amyloid precursor protein; APP;		
KW	beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syndrome;		
KW	HCHMA-D; Swedish mutation; maltose binding protein; MBP.		
XX			
OS	Homo sapiens.		
XX			
PN	US6221645-B1.		
XX			
PD	24-APR-2001.		
XX			

PF	07-JUN-1996;	96US-0660531.
XX		
PR	07-JUN-1995;	95US-0480498.
XX		
PA	(ELAN-) ELAN PHARM INC.	
PI	Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;	
XX		
DR	WPI: 2001-315578/33.	
XX		
PT	Novel antibody that specifically binds native beta-secretase protein,	
PR	useful for raising anti-idiotypic antibodies and for detecting or	
PT	diagnosing pathological conditions related to presence of respective	
PT	antigens -	
XX		
PS	Example; Column 28; 42pp; English.	
XX		
CC	The sequences given in AAB47260-61 represent cleavage sites derived	
CC	from wild-type and the Swedish mutation of beta-amyloid precursor	
CC	protein (APP). These cleavage sites were used in fusion proteins	
CC	which were used as substrates for the beta-secretase protein which	
CC	is characterized by an ability to cleave the 695-amino acid isoctype	
CC	of APP between amino acids 596 and 597. The fusion proteins contain	
CC	the carboxy-terminal end of Maltose binding protein (MBP) fused to	
CC	the carboxy-terminal 125 amino acids of either wild type APP or APP	
CC	containing the Swedish mutation. Beta-secretase is thought to be	
CC	responsible for the pathogenic processing of APP to form beta amyloid	
CC	peptide (beta-AP) in beta-AP related conditions, e.g. Alzheimer's	
CC	disease, Downs syndrome, HCHWA-D etc. Beta-secretase has a molecular	
CC	weight of 260-300 kd and will bind to wheat germ agglutinin but not to	
CC	concanavalin A. Beta-secretase will cleave both the wild type and	
CC	the Swedish mutation of APP.	
SQ	Sequence 5 AA:	
	Query Match 100.0%; Score 20; DB 22; Length 5;	
	Best Local Similarity 100.0%; Pred. No. 7.8e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 NLDA 4	
DB	2 NLDA 5	
	RESULT 10	
ID	AU078500 standard; Peptide: 6 AA.	
AC	AU078500	
XX		
AC	AU078500;	
XX		
DT	18-JUN-2002 (first entry)	
XX		
DE	Beta secretase cleavage site of beta APP Swedish mutant.	
XX		
KM	Alzheimer's disease; APP; beta amyloid precursor protein; beta secretase;	
KM	BACE; beta-site APP cleaving enzyme; human; neurotrophic; neuroprotective;	
KM	beta-site amyloid precursor protein (APP)-cleaving enzyme;	
KM	BACE secretase/shedase; neurodegenerative disorder.	
XX		
OS	Homo sapiens.	
XX		
FH	Key Location/Qualifiers	
FT	Cleavage-site 4..5	
FT	/note= "Beta secretase cleavage site"	
XX		
PN	WO200210354-A2.	
XX		
PD	07-FEB-2002.	
XX		
PE	01-AUG-2001; 2001WO-CA01118.	
XX		
PX	01-AUG-2000; 2000CA-2313828.	
PR		
XX		

PA	(RECL-) INST RECH CLINIQUES MONTREAL.
PI	Seidah NG, Chretien M, Cromlish JA;
XX	
XX	WPI; 2002-280632/32.
DR	
XX	
PT	Modulating activity of beta-site amyloid precursor protein-cleaving
PT	enzyme secretase/shedase for treatment of neurodegenerative disorder
PT	characterised by generation of Abeta protein, by preventing cleavage of
PS	enzyme -
PS	Disclosure; Page 2; 64pp; English.
CC	This invention relates to a novel method for modulating activity of
CC	beta-site amyloid precursor protein (APP)-cleaving enzyme (BACE)
CC	secretase/shedase. Cleavage of BACE by this enzyme results in the
CC	generation of a soluble BACE which enhances the production of the
CC	amyloidogenic peptide Abeta which has been shown to be involved in the
CC	aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
CC	achieved by administration of an antisense nucleotide molecule capable
CC	of hybridising with BACE mRNA, by using a ribozyme that targets and
CC	degrades BACE secretase mRNA, with a peptide that can interfere with
CC	binding of the enzyme with BACE or using an antibody or antagonist that
CC	can function as an inhibitor of BACE secretase activation. The methods
CC	of the invention modulate the activity of BACE secretase/shedase by
CC	preventing cleavage of BACE, which is useful for the treatment of a
CC	neurodegenerative disorder characterised by the generation of Abeta
CC	protein, especially Alzheimer's disease. The invention also comprises a
CC	method for identification of an agent that can alter the ability of BACE
CC	secretase to associate with and process a known substrate, this method
CC	can be used for high throughput screening of candidate molecules. The
CC	invention also comprises a method for determining whether an individual
CC	is at risk of developing a neurodegenerative disorder characterised
CC	by the generation of Abeta protein by measuring the levels of BACE
CC	C terminal cleavage products in a sample or tissue where an increase
CC	in cleavage products indicates a person at risk. The present sequence
CC	represents the beta secretase cleavage site of the Swedish mutant of
CC	beta amyloid precursor protein.
SQ	Sequence 6 AA;
OY	Query Match 100.0%; Score 20; DB 23; Length 6;
DB	Best Local Similarity 100.0%; Pred. No. 7.B+05;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 NIDA 4
	3 NIDA 6
RESULT 11	
ID	AA94771 standard; Protein; 8 AA.
AY94771	
AA94771:	
DT	12-FEB-2001 (first entry)
DE	Beta-secretase substrate peptide SEQ ID 17.
XX	
XX	Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;
KW	Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.
XX	
OS	Synthetic.
PN	MO200058479-A1.
PD	05-OCT-2000.
PF	23-MAR-2000; 2000WO-US07755.
RR	26-MAR-1999; 99US-0277229.

[illegible]

PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
PI Blenkowski MJ, Gurney M;
DR WPI: 2001-444208/48.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity for identifying modulators useful in treating Alzheimer's
PT disease -
XX
PS Example 15; Page 92; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human aspartyl
CC protease-1 (hu-Asp-1) beta-secretase Swedish (Sw) mutant peptide
CC which is used for determining the enzymatic activity of Asp-1 protein
CC lacking a transmembrane (TM) domain and containing (His)6 tag.
XX
SQ Sequence 8 AA:
OY 1 NLDA 4
 ||||
 3 NLDA 6
Db
Query Match 100.0%; Score 20; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
RESULT 13
AAE02613
ID AAE02613 standard; peptide; 8 AA.
XX
AC AAE02613;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human Aspartyl protease-1 beta-secretase Swedish mutant form peptide.
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antiAlzheimer's; aspartyl protease 1; Asp1;
KW beta-secretase.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 4..5
XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26080.
XX

PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
PI Gurney M, Blenkowski MJ;
DR WPI: 2001-290516/30.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
PS Example 15; Page 94; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
CC (hu-Asp-1) beta-secretase, Swedish (Sw) mutant form peptide which is used
CC for determining the enzymatic activity of Asp-1 deltatm (His)6 protein.
XX
SQ Sequence 8 AA:
OY 1 NLDA 4
 ||||
 3 NLDA 6
Db
Query Match 100.0%; Score 20; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
RESULT 14
ABB78622
ID ABB78622 standard; Peptide; 8 AA.
XX
AC ABB78622;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human beta secretase peptide SEQ ID NO:71.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
PI Blenkowski MJ, Gurney M;
DR WPI: 2002-396337/43.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect
PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
PT disease -

XX Example 15; Page 92; 182pp; English.

PS The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see AB152456) where the nucleotide sequence encodes a polypeptide having
 CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see AB378589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease or
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents a human beta secretase peptide, which is used in
 CC an example from the present invention.

CC Sequence 8 AA;

Query Match 100.0%; Score 20; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
 ||||
 DB 3 NIDA 6

RESULT 15

AAW82081 ID AAW82081 standard; peptide; 9 AA.

AAW82081;

18-FEB-1999 (first entry).

Fluorogenic protease indicator protease binding peptide #59.

Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
 conformation change.

Synthetic.

WO9837226-A1.

27-AUG-1998.

20-FEB-1998; 98WO-US03000.

20-FEB-1997; 97US-0802981.

(ONCO-) ONCOIMMUNIN INC.

Komoriya A, Packard BS.

WPI; 1998-467579/40.

New fluorogenic compositions - containing 2 fluorophores separated
 by a peptide comprising a protease binding site, used for detecting
 protease activity in samples.

Claim 4; Page 77; 90pp; English.

XX AAW82023-W82240 are peptides used in the construction of a fluorogenic
 CC composition which is used for the detection of protease activity in
 CC biological samples. The products can be used for the detection of
 CC conformation changes in nucleic acids, oligosaccharides,
 CC polysaccharides, proteins, peptides, lipids, phospholipids, glycolipids,
 CC glycoproteins, steroids or polymers. In addition, attachment of a
 CC hydrophobic group to a molecule can be used to enhance uptake by cells.
 CC The composition is composed of P = 'peptide comprising a protease binding
 CC site for the protease, F1, F2 peptides = fluorophores where F1 is
 CC attached to the amino terminal amino acid and F2 is attached to the
 CC carboxyl terminal amino acid and S1, S2 peptides = when present, are
 CC peptide spacers where S1, when present, is attached to the amino terminal
 CC acid, and S2, when present, is attached to the carboxyl terminal amino
 CC acid.

CC Sequence 9 AA;

Query Match 100.0%; Score 20; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
 ||||
 DB 4 NIDA 7

RESULT 16

AAW87874 ID AAW87874 standard; peptide; 9 AA.

AAW87874;

14-NOV-2000 (first entry)

A peptide fragment derived from beta-amyloid precursor protein.

Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 inhibitor.

Homo sapiens.

WO200047618-A2.

17-AUG-2000.

10-FEB-2000; 2000WO-US03819.

10-FEB-1999; 99US-0119571.

15-JUN-1999; 99US-0139172.

(ELAN-) ELAN PHARM INC.

Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

WPI; 2000-533011/48.

Purified beta-secretase protein used in assays to discover inhibitors
 which can be used for the treatment of amyloidogenic diseases e.g.
 Alzheimer's disease -

Disclosure; Page 12; 121pp; English.

The specification describes a beta-secretase enzyme. The enzyme cleaves
 beta-amyloid precursor protein to produce beta-amyloid peptide. This
 enzyme is therefore implicated in the production of amyloid plaque
 components which accumulate in the brains of individuals afflicted with
 Alzheimer's disease. Inhibitors of beta-secretase are administered to
 a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
 disease-like pathology to test if they maintain or improve cognitive
 ability or reduce the plaque burden. The compounds are used for the

CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
 CC present sequence represents a peptide derived from beta-amyloid
 CC precursor protein
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 4 NLDA 7

RESULT 17
 AAB07894
 ID AAB07894 standard; Peptide; 9 AA.
 XX
 AC AAB07894;

DT 14-NOV-2000 (first entry)
 XX

DE Substrate for beta-secretase enzyme.
 XX

KM Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KM amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW Inhibitor.
 XX

OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 XX

PN WO200047618-A2.
 XX

PD 17-AUG-2000.
 XX

PF 10-FEB-2000; 2000WO-US03819.
 XX

PR 10-FEB-1999; 99US-0119571.
 PR 15-JUN-1999; 99US-0139172.
 XX

PA (ELAN-) ELAN PHARM INC.
 XX

PI Anderson JP, Basl G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
 XX
 DR WPI; 2000-533011/48.

PT Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease -
 XX

PS Example 4; Page 71; 121pp; English.
 XX

CC The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
 CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
 CC disease-like pathology to test if they maintain or improve cognitive
 CC ability or reduce the plaque burden. The compounds are used for the
 CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
 CC present sequence represents a peptide substrate used to test the
 CC activity of beta-secretase enzyme.
 CC

SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 4 NLDA 7

RESULT 18
 AAG73297
 ID AAG73297 standard; Peptide; 9 AA.
 XX
 AC AAG73297;

DT 14-AUG-2001 (first entry)
 XX

DE Protease indicator compound peptide #26.
 XX

KM Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KM viral infection; cancer metastasis; emphysema; arthritis;
 KW thrombosis; haemophilia.
 XX

OS Synthetic.
 XX

PN WO200118238-A1.
 XX

PD 15-MAR-2001.
 XX

PF 11-SEP-2000; 2000WO-US24882.
 XX

PR 10-SEP-1999; 99US-0394019.
 XX

PA (ONCO-) ONCOMMUNIN INC.
 XX

PI Komoriya A, Packard BS;
 XX

DR WPI; 2001-389573/41.
 XX

PT New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples -
 XX
 PS Claim 1; Page 70; 86pp; English.
 XX

CC The present invention describes fluorogenic compositions which can be
 CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention.
 CC

SQ Sequence 9 AA;

Query Match 100.0%; Score 20; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 4 NLDA 7

RESULT 19
 ABB09003
 ID ABB09003 standard; peptide; 9 AA.
 XX
 AC ABB09003;

DT 19-JUN-2002 (first entry)
 XX

DE Peptide #1 used as a tag to identify cleavage products.
 XX

KM Amyloid precursor protein; APP; Alzheimer's disease; neurotropic;
 KM neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;
 KM Down's syndrome; cerebral amyloid angiopathy; dementia.
 OS Synthetic.
 XX
 XX
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 FT /note="Beta secretase cleavage site"
 XX
 XX
 PN WO200202505-A2.
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US20852.
 XX
 PR 30-JUN-2000; 2000US-215323P.
 XX
 PA (ELAN) ELAN PHARM INC.
 PI Fang IX, Hom R, John V, Mallalard M;
 DR WPI; 2002-171625/22.
 XX
 XX
 PT New substituted amines are e.g. beta-amyloid peptide inhibitors, useful
 PT for treating Alzheimer's disease, mild cognitive impairment and Down's
 PT syndrome -
 XX
 XX
 PS Example D; Page 96; 136pp; English.
 XX
 XX This invention relates to substituted amines and their salts, which
 CC are neurotropic, neuroprotective, cerebroprotective, haemostatic and
 CC antiparkinsonian in their action. They are used in the preparation of
 CC a composition useful for treating, preventing or delaying the on-set
 CC of Alzheimer's disease, for treating mild cognitive impairment, Down's
 CC syndrome, cerebral amyloid angiopathy, dementia associated with
 CC Parkinson's disease, dementia associated with progressive supranuclear
 CC palsy, and dementia associated with cortical basal degeneration.
 CC They are also useful for treating diseases characterised by beta-amyloid
 CC deposits in brain, and for producing beta-secretase complexes. This
 CC sequence represents a peptide that incorporate the known cleavage
 CC site of beta-secretase. This substrate is used to assay
 CC beta-secretase activity.
 CC
 SO Sequence 9 AA;
 QY
 DB 1 NLDA 4
 DB 4 NLDA 7
 RESULT 20
 ABB06519
 ID ABB06519 standard; Peptide; 9 AA.
 XX
 AC ABB06519;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 XX Beta-secretase related peptide SEQ ID NO:113.
 XX
 XX Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KM aspartyl protease; neuroprotective; neurotropic; beta-secretase inhibitor;
 KM Alzheimer's disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200206306-A2.

XX
 PD 24-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US23035.
 XX
 PR 19-JUL-2000; 2000US-219795P.
 PR 12-MAR-2001; 2001US-275251P.
 XX
 PA (PHARMA) PHARMACIA & UPJOHN CO.
 PI Yan R, Tomasselli AG, Gurney ME,
 PI Heinrichson RL, Emmons TL, Bienkowski MJ;
 DR WPI; 2002-216995/27.
 XX
 XX
 PT Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease -
 XX
 PS Disclosure; Page 156; 188pp; English.
 XX
 XX The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC neurotropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. AB149514 to AB149525 and
 CC AB06409 to AB06593 represent sequences used in the exemplification
 CC of the present invention.
 CC
 SO Sequence 9 AA;
 QY
 DB 1 NLDA 4
 DB 3 NLDA 6
 RESULT 21
 AAM50897
 ID AAM50897 standard; Peptide; 9 AA.
 XX
 AC AAM50897;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 XX Oligopeptide substrate for beta-secretase.
 XX
 XX Beta-secretase; substrate; amyloid precursor protein;
 KM APP; amyloid beta peptide; inhibitor; screening;
 KM neurodegenerative disorder; cognitive impairment; Down's syndrome;
 KM Alzheimer's disease; hereditary cerebral haemorrhage;
 KM cerebral amyloid angiopathy; dementia; therapy.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 FT
 XX
 PN WO200202512-A2.
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21012.

XX	30-JUN-2000;	2000US-215323P.
PR	22-NOV-2000;	2000US-252736P.
PR	15-DEC-2000;	2000US-253956P.
PR	13-FEB-2001;	2001US-268497P.
PR	29-MAR-2001;	2001US-279779P.
PR	04-JUN-2001;	2001US-295589P.
XX		
PA	(ELAN-) ELAN PHARM INC.	
PA	(PHAA) PHARMACIA & UPJOHN CO.	
PI	Malilaard M, Hom C, Gallunas A,	Jagodzinska B, Fang LY, John V,
PI	Freskos JN, Pulley SR, Beck JP,	Tenbrink RE;
XX		
XX	WPI; 2002-171627/22.	
DR		
XX		
PT	New substituted amines are e.g. amyloid beta peptide production	
PT	inhibitors, useful for treating or preventing e.g. Alzheimer's disease,	
PT	mild cognitive impairment and other degenerative diseases -	
XX		
PS	Example D; Page 344; 651pp; English.	
XX		
CC	The present sequence is that of a peptide that incorporates the	
CC	known cleavage site of beta-secretase on amyloid precursor protein	
CC	(APP). The peptide, which may optionally be tagged with a	
CC	fluorescent or chromogenic moiety, can be used in assays to	
CC	determine the beta-secretase inhibitory activity of novel	
CC	substituted amine compounds of the invention. Comparison of	
CC	substrate cleavage results in the presence of an inhibitor and	
CC	in the presence of a control provides a measure of the compound's	
CC	inhibitory activity. Novel compounds of the invention are	
CC	effective inhibitors of beta-secretase, inhibit beta-secretase	
CC	mediated cleavage of APP, are effective inhibitors of A beta	
CC	production, and/or effectively reduce amyloid beta deposits or	
CC	plaques. They are used in the treatment or prevention of diseases	
CC	characterised by amyloid deposits in the brain, e.g. for treating	
CC	or preventing Alzheimer's disease (AD), for helping prevent or	
CC	delay the onset of AD, for treating mild cognitive impairment	
CC	(MCI), preventing or delaying the onset of AD in those who would	
CC	progress from MCI to AD, for treating Down's syndrome and	
CC	hereditary cerebral haemorrhage with Amyloidosis of the Dutch	
CC	type, for treating cerebral amyloid angiopathy and preventing its	
CC	potential consequences i.e. single and recurrent lobar haemorrhages,	
CC	for treating other degenerative dementias, including dementias	
CC	of mixed vascular and degenerative origin, dementia associated with	
CC	Parkinson's disease, dementia associated with progressive	
CC	supranuclear palsy, and dementia associated with cortical basal	
CC	degeneration, and for treating diffuse Lewy body type of AD (all	
CC	claimed).	
CC		
XX		
SO	Sequence 9 AA:	
	Query Match 100.0%; Score 20; DB 23; Length 9;	
	Best Local Similarity 100.0%; Pred. NO. 7.0e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 NLDA 4	
DB	4 NLDA 7	
RESULT 22		
ID	ABB07598	
XX	ABB07598 standard; peptide: 9 AA.	
XX	ABB07598;	
XX		
DT	08-MAY-2002 (first entry)	
XX		
DE	Synthetic oligopeptide substrate having beta-secretase cleavage site.	
XX		
KW	APP; amine derivative; beta-secretase; amyloid precursor protein; A beta;	
KW	amyloid beta peptide; beta-amyloid; neurotropic; neuroprotective;	

KM	cerebroprotective; haemostatic; antiparkinsonian.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	5..6
FT	Cleavage-site
XX	/note= "beta-secretase cleavage site"
PN	WO200202520-A2.
XX	
PD	10-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-US21000.
XX	
PR	30-JUN-2000; 2000US-215323P.
PR	29-JUN-2001; 2001US-0895843.
XX	
PA	(ELAN-) ELAN PHARM INC.
PA	(PHAA) PHARMACIA & UPJOHN CO.
PI	Beck JP, Gallunas A, Hom R, Jagodzinska B, John V, Maillard M;
XX	
DR	WPI: 2002-188416/24.
XX	
PT	New disubstituted amine derivatives, useful for treating Alzheimer's
PT	disease and other degenerative diseases -
XX	
PS	Example D: Page 163; 266pp: English.
XX	
CC	The invention relates to disubstituted amine derivatives of specified
CC	formulae or their salts. The amine derivatives can inhibit beta-secretase
CC	activity or inhibit the cleavage of amyloid precursor protein (APP) in a
CC	reaction mixture. They can also be used to inhibit production of amyloid
CC	beta peptide (A beta) in a cell or inhibit production of beta-amyloid
CC	plaque in an animal. The amine derivatives are useful for treating or
CC	preventing a disease characterized by beta-amyloid deposits in the brain
CC	e.g. for treating or preventing Alzheimer's disease (AD), for helping
CC	prevent or delay the onset of AD, for treating mild cognitive impairment
CC	(MCI), preventing or delaying the onset of AD in those who would progress
CC	from MCI to AD, for treating Down's syndrome, humans who have hereditary
CC	cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
CC	amyloid angiopathy and preventing its potential consequences i.e. single
CC	and recurrent lobar haemorrhages, for treating other degenerative
CC	dementias, including dementias of mixed vascular and degenerative origin,
CC	dementia associated with Parkinson's disease, dementia associated with
CC	progressive supranuclear palsy, dementia associated with cortical basal
CC	degeneration, diffuse Lewy body type of Alzheimer's disease. Sequences
CC	AB807598-599 are synthetic APP oligopeptide substrates containing the
CC	cleavage site of beta-secretase, used to assay beta-secretase activity.
XX	
SQ	Sequence 9 AA:
QY	1 NDA 4
DB	4 NDA 7
XX	
RESULT 23	
AAEL16663	
ID	AAEL16663 standard; peptide; 9 AA.
XX	
AC	AAEL16663;
XX	
DT	09-APR-2002 (first entry)
XX	
DE	Oligopeptide substrate #1, used in the assay of the invention.
XX	
KM	Disubstituted amine derivative; Alzheimer's disease; Down's syndrome;
KM	degenerative disease; beta-amyloid deposit; mild cognitive impairment;

KW hereditary cerebral haemorrhage; amyloidosis; degenerative dementia;
 KW cerebral amyloid angiopathy; Parkinson's disease; supranuclear palsy;
 KW cortical basal degeneration; AD; MCI; amyloid precursor protein;
 KW beta-secretase; amyloid beta peptide; A beta peptide.
 OS Unidentified.
 XX
 XX
 FT Key Location/Qualifiers
 FT Cleavage-site 5..6
 PN WO200202518-A2.
 XX 10-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US20856.
 XX
 XX 30-JUN-2000; 2000US-215323P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 XX (PHAA-) PHARMACIA & UPJOHN CO.
 XX
 XX Beck JP, Gallunas A, Hom R, Jagodzinska B, John V, Malliaird M;
 XX WPI; 2002-122550/16.
 XX
 XX New substituted amine derivatives, useful for treating Alzheimer's
 XX disease and other degenerative diseases -
 XX
 XX Example D; Page 163; 286pp; English.
 XX
 XX The invention relates to substituted amine derivative compounds
 XX useful for treating Alzheimer's disease and other degenerative diseases.
 XX Compounds of the invention possess beta secretase inhibitory activity and
 XX are useful for inhibiting beta-secretase mediated cleavage of amyloid
 XX precursor protein (APP) and particularly, to inhibit the production of
 XX amyloid beta (A beta) peptide. They are useful for treating or preventing
 XX a disease characterised by beta-amyloid deposits in the brain e.g. for
 XX treating or preventing Alzheimer's disease (AD), for helping to prevent
 XX or delay the onset of Alzheimer's disease, for treating mild cognitive
 XX impairment (MCI), Down's syndrome, hereditary cerebral haemorrhage with
 XX the amyloidosis of the Dutch type, cerebral amyloid angiopathy and
 XX preventing its potential consequences i.e. single and recurrent lobar
 XX haemorrhages, for treating other degenerative dementias including
 XX dementias of mixed vascular and degenerative origin, dementia associated
 XX with Parkinson's disease, dementia associated with progressive
 XX supranuclear palsy, dementia associated with cortical basal degeneration
 XX and diffuse Lewy body type of Alzheimer's disease. The present sequence
 XX is oligopeptide substrate used in assay of the invention.
 SQ Sequence 9 AA;
 QY Query Match 100.0%; Score 20; DB 23; Length 9;
 Db Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLDA 4
 Db 4 NLDA 7
 RESULT 24
 ID AAU74837 standard; Peptide; 9 AA.
 AC AAU74837;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Synthetic amyloid precursor protein (APP) oligopeptide substrate #1.
 XX
 KW Amyloid precursor protein; APP; Alzheimer's disease; amine XY;
 KW neurotrophic; neuroprotective; cerebroprotective; haemostatic;
 KW antiparkinsonian; beta-secretase; amyloid beta peptide; amyloidosis;

KW beta-amyloid plaque; mild cognitive impairment; MCI; Down's syndrome;
 KW hereditary cerebral haemorrhage; cortical basal degeneration;
 KW cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;
 KW Parkinson's disease; supranuclear palsy; dementia.
 OS Synthetic.
 XX
 XX
 FT Key Location/Qualifiers
 FT Cleavage site 5..6
 FT /note= "Beta-secretase cleavage site"
 PN WO200202506-A2.
 XX 10-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US20930.
 XX
 XX 30-JUN-2000; 2000US-215323P.
 XX
 XX (ELAN-) ELAN PHARM INC.
 XX
 XX Fang LY, John V;
 XX WPI; 2002-147995/19.
 XX
 XX New substituted amines are e.g. amyloid beta peptide production
 XX inhibitors, useful for treating or preventing e.g. Alzheimer's disease,
 XX mild cognitive impairment and other degenerative diseases -
 XX
 XX Example D; Page 118; 434pp; English.
 XX
 XX This invention relates to a novel substituted amine of formula XV and
 XX its salts which can be used to treat Alzheimer's disease and similar
 XX diseases. The compound of the invention may have neurotrophic,
 XX neuroprotective, cerebroprotective, haemostatic and antiparkinsonian
 XX activities. The amine acts as a beta-secretase activity inhibitor,
 XX inhibiting cleavage of amyloid precursor protein (APP) and the
 XX formation of amyloid beta peptide and beta-amyloid plaque production.
 XX The amine of the invention is useful for treating or preventing a
 XX disease characterised by beta-amyloid deposits in the brain e.g.
 XX Alzheimer's disease (AD), for treating mild cognitive impairment (MCI),
 XX preventing or delaying the onset of Alzheimer's disease in those who
 XX would progress from MCI to AD, for treating Down's syndrome, humans who
 XX have hereditary cerebral haemorrhage with the Amyloidosis of the Dutch
 XX type, cerebral amyloid angiopathy and preventing its potential
 XX consequences i.e. single and recurrent lobar haemorrhages, for treating
 XX other degenerative dementias, including dementias of mixed vascular and
 XX degenerative origin, dementia associated with Parkinson's disease,
 XX dementia associated with progressive supranuclear palsy, dementia
 XX associated with cortical basal degeneration and diffuse Lewy body type
 XX of Alzheimer's disease. The present sequence represents a synthetic
 XX APP oligopeptide substrate #1 for the beta secretase enzyme. This
 XX is a synthetic substrate was used to test the efficiency of the amine as an
 XX inhibitor of beta secretase enzyme activity.
 SQ Sequence 9 AA;
 QY Query Match 100.0%; Score 20; DB 23; Length 9;
 Db Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLDA 4
 Db 4 NLDA 7
 RESULT 25
 ID AAM08362 standard; peptide; 10 AA.
 AC AAM08362;
 XX
 DT 05-SEP-1997 (first entry)


```

XX DE Beta-secretase substrate #3.
XX KW Beta-cleavage site: beta amyloid precursor protein; APP; beta-secretase;
XX KM alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
XX OS Synthetic.
XX FT
XX FT Key Location/Qualifiers
XX FT Misc-difference 1 /note="acetylated"
XX PN W09640885-A2.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-0509985.
XX PR 07-JUN-1995; 95US-0485152.
XX PR 07-JUN-1995; 95US-0480498.
XX PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
XX PI Mcconlogue LC, Sinha S, Tan H;
XX DR WPI; 1997-052304/05.
XX PT Beta-secretase which specifically cleaves beta-amyloid precursor
XX PT protein - useful to screen for inhibitors useful in treatment of
XX PT Alzheimer's disease
XX PS Disclosure; Page 45; 92pp; English.
XX CC AA008359-W08362 represent substrates for the enzyme of the invention.
XX CC The enzyme of the invention is beta-secretase, and specifically cleaves
XX CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP
XX CC is thought to occur via cleavage between residues 16 and 17 of the
XX CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing
XX CC is thought to occur by beta-secretase cleavage of beta-APP.
XX CC Beta-secretase activity can be detected and measured using a method of
XX CC the invention, which detects at least one of the beta-secretase cleavage
XX CC products formed on cleavage. The method can be used to determine whether
XX CC a test substance inhibits proteolytic cleavage, by beta-secretase, of
XX CC beta-APP. Compounds effective to at least partially inhibit
XX CC beta-secretase activity can be used to inhibit cleavage of beta-APP in
XX CC cells or mammalian hosts. Isolation and purification of beta-secretase
XX CC will permit chemical modelling of a critical event in the pathology of
XX CC Alzheimer's disease.
XX SQ Sequence 10 AA;
XX
XX Query Match 100.0%; Score 20; DB 18; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 92;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NLDA 4
XX ||||
XX DB 4 NLDA 7
XX
XX RESULT 26
XX AA33756
XX ID AAY33756 standard; Protein; 10 AA.
XX AC AAY33756;
XX AC
XX DT 09-NOV-1999 (first entry)
XX XX
XX DE Synthetic oligopeptide 5-5'SW.
XX XX
XX KM Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
XX KM Alzheimer's disease; measure activity; cleavage site.

```

```

XX OS Synthetic.
XX FT
XX FT Key Location/Qualifiers
XX FT Modified-site 1 /note="N-terminal Ser is acetylated"
XX PN US5942400-A.
XX PD 24-AUG-1999.
XX PF 07-JUN-1996; 96US-0659984.
XX PR 07-JUN-1996; 96US-0659984.
XX PR 07-JUN-1995; 95US-0480498.
XX PR 07-JUN-1995; 95US-0485152.
XX PA (ELAN-) ELAN PHARM INC.
XX PI Anderson JP, Jacobson-Croak KL, Sinha S;
XX PI WPI; 1999-517417/43.
XX DR
XX PT A method for detecting human beta-secretase cleavage of polypeptides
XX PT useful for identifying beta-secretase inhibitors
XX PS Examples; Column 30; 43pp; English.
XX CC Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring
XX CC the activity of beta-secretase (AAY33741). Beta-secretase is capable of
XX CC cleaving beta-amyloid protein precursor (APP) (AAY33742). These
XX CC synthetic peptides contain the cleavage site of APP. Beta-secretase and
XX CC APP are used in a method for detecting human beta-secretase cleavage of
XX CC polypeptides and for identifying beta-secretase inhibitors. Inhibition
XX CC of beta-secretase activity would be useful for chemical modelling of a
XX CC critical event in the pathology of Alzheimer's disease. Inhibitors of
XX CC beta-secretase would be useful for the prevention and treatment of
XX CC Alzheimer's disease and Down's Syndrome.
XX SQ Sequence 10 AA;
XX
XX Query Match 100.0%; Score 20; DB 20; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 92;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 NLDA 4
XX ||||
XX DB 4 NLDA 7
XX
XX RESULT 27
XX AA69707
XX ID AAY69707 standard; peptide; 10 AA.
XX AC AAY69707;
XX AC
XX DT 11-APR-2000 (first entry)
XX XX
XX DE Beta-APP alpha-secretase substrate [NLD]-APP(-5,+5).
XX XX
XX KM Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX KM cleavage site: beta-secretase; neurodegenerative disease;
XX KM Alzheimer's disease.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN W09964587-A1.
XX PD 16-DEC-1999.
XX PF 04-JUN-1999; 99WO-FR01326.
XX XX

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PR 05-JUN-1998; 98PR-0007068.
 PR 31-MAR-1999; 99US-0122599.
 XX
 PA (RHON) RHONE-POULENC RORER SA.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.
 XX
 PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
 XX WPI: 2000-097537/08.
 DR
 XX Polypeptide with beta-secretase activity, specific for wild-type
 PT amyloid precursor protein, useful in treating Alzheimer's disease -
 XX
 PS Example 3; Page 24; 44pp; French.
 CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
 CC novel polypeptide with beta-secretase activity that can cleave
 CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
 CC polypeptide is used to identify agents that interact specifically with
 CC it. These agents regulate metabolism of APP, particularly they slow down
 CC or reduce production of beta-amyloid, so can be used to treat
 CC neurodegenerative diseases, particularly Alzheimer's disease.
 CC
 XX Sequence 10 AA:

Query Match 100.0%; Score 20; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NLDA 4
 Db 4 NLDA 7

RESULT 28
 AAE10653
 ID AAE10653 standard; peptide: 10 AA.
 XX
 AC AAE10653;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human APP-Sw beta-secretase substrate peptide mutant, PHA-247574E.
 XX
 KW Human: aspartyl protease 1; Aspl; amyloid precursor protein;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
 KW APP-Sw beta-secretase peptide; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 4
 FT Misc-difference 5 /note= "Wild type Lys substituted with Asn"
 FT Misc-difference 5 /note= "Wild type Met substituted with Leu"
 FT Cleavage-site 5..6
 XX
 XX GR2357767-A.
 PN
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-0023315.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WD-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX

PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Bienkowski MJ, Gurney M;
 XX
 DR WPI: 2001-444208/48.
 XX
 XX Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 PS Example 12; Page 84; 187pp; English.

XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
 CC Aspl proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Aspl alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Aspl alpha-secretase activity, where modulators that increase
 CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
 CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Aspl proteolytic activity. The present sequence is human amyloid
 CC precursor protein-Swedish (APP-Sw) beta-secretase specific substrate
 CC peptide mutant, PHA-247574E. This peptide is obtained by Swedish
 CC KM-NL mutation. This peptide is used for assaying the beta-secretase
 CC activity of human Aspartyl protease 2a (Asp2a) protein. The peptide
 CC is also used for determining the relationship between Aspl and
 CC APP protein.
 CC
 XX Sequence 10 AA:

Query Match 100.0%; Score 20; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NLDA 4
 Db 4 NLDA 7

RESULT 29
 AAE06898
 ID AAE06898 standard; peptide: 10 AA.
 XX
 AC AAE06898;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Human amyloid precursor protein (APP-Sw) beta-secretase peptide #1.
 XX
 KW Human: aspartyl protease 2; Asp 2; beta-amyloid precursor protein;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
 KW neuroprotective; antisense therapy; APP-Sw; gene therapy.
 XX
 OS Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 5..6
 FT
 FT
 PN WO200150829-A2.
 XX
 XX 19-JUL-2001.
 PD
 XX 09-MAY-2001; 2001WO-IB00799.
 PF
 XX 09-MAY-2001; 2001WO-IB00799.
 PR
 XX

PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
DR WPI: 2001-463072/52.
XX
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Claim 10: Page 84; 185pp; English.
XX
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is human amyloid precursor protein (APP-SW)
CC beta-secretase peptide related to the invention.
XX
SQ Sequence 10 AA:
OY 1 NLDA 4
Db 4 NLDA 7
Query Match 100.0%; Score 20; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 30
AAU06627
ID AAU06627 standard; Peptide: 10 AA.
XX
AC AAU06627;
XX
DT 24-OCT-2001 (first entry)
XX
DE Synthetic Asp2 recognition site from APP-SW.
XX
KM Aspartyl protease; Asp2; beta-secretase; neurotropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KM amyloid-beta; Abeta; APP-SW.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 5 /label= Asp2_protease_cleavage_site
XX
PN WO200149098-A2.
XX
PD 12-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-IB00798.
XX
XX 09-MAY-2001; 2001WO-IB00798.
PR

XX
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
DR WPI: 2001-502549/55.
XX
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
XX Claim 10: Page 84; 185pp; English.
XX
XX The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp2) protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC protein and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-SW-beta-secretase peptide sequence (NLDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating to Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridize to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is an synthetic
CC peptide substrate for Asp2 corresponding to the APP Swedish mutation
CC site, APP-SW.
XX
SQ Sequence 10 AA:
OY 1 NLDA 4
Db 4 NLDA 7
Query Match 100.0%; Score 20; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 31
AAU07226
ID AAU07226 standard; Peptide: 10 AA.
XX
AC AAU07226;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human beta-amyloid protein precursor, APP-SW beta-secretase site.
XX
KM Human; aspartyl protease 1; Asp-1; neurotropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
KW beta-secretase; Alzheimer's disease; APP-SW.
XX
OS Homo sapiens.
XX
XX WO200149097-A2.
XX


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PF 07-JUN-1996; 96US-0660531.
XX
PR 07-JUN-1995; 95US-0480498.
XX
XX (ELAN-) ELAN PHARM INC.
XX
PI Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;
DR WPI; 2001-315578/33.
XX
XX Novel antibody that specifically binds native beta-secretase protein,
PT useful for raising anti-idiotypic antibodies and for detecting or
PT diagnosing pathological conditions related to presence of respective
PT antigens
XX
PS Example; Column 30; 42pp; English.
XX
XX The sequences given in AAB47262-67 represent synthetic peptides
CC containing the cleavage sites derived from wild-type beta-amyloid
CC precursor protein (APP). These peptides were used in assays utilizing
CC partially purified beta-secretase to identify beta-secretase inhibitors.
CC Beta-secretase is thought to be responsible for the pathogenic
CC processing of APP to form beta amyloid peptide (beta-A $\beta$ ) in beta-AP
CC related conditions, e.g. Alzheimer's disease, Downs syndrome, HCHWA-D
CC etc. Beta-secretase has a molecular weight of 260-300 kD and will bind
CC to wheat germ agglutinin but not to concanavalin A. Beta-secretase
CC will cleave both the wild type and the Swedish mutation of APP.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
   ||||
Db 4 NIDA 7

RESULT 34
AAB6575
ID AAB6575 standard; Peptide; 10 AA.
XX
AC AAB6575;
XX
XX 12-APR-2001 (first entry)
XX
DE Synthetic peptide derived from APP beta-secretase site.
XX
KW Memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
KW APP; memapsin 2 inhibitor; Alzheimer's disease.
XX
OS Synthetic.
XX
XX WO200100665-A2.
XX
XX 04-JAN-2001.
XX
XX 27-JUN-2000; 2000WO-US17742.
XX
XX 28-JUN-1999; 99US-0141363.
XX 30-NOV-1999; 99US-0168060.
XX 25-JAN-2000; 2000US-0177836.
XX 27-JAN-2000; 2000US-0178368.
XX 08-JUN-2000; 2000US-0210292.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX (UNITI ) UNIV ILLINOIS FOUND.
XX
XX Tang JUN, Hong L, Ghosh AK;
XX
XX WPI; 2001-137933/14.
XX

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```

PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
PT having 2 catalytic aspartic residues and substrate binding cleft, used
PT to treat Alzheimer's disease by blocking amyloid precursor protein
PT cleavage
XX
XX Disclosure; Page 11; 86pp; English.
XX
XX The present sequence is given in a specification relating to an inhibitor
CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
CC active site, which is defined by the presence of two catalytic aspartic
CC residues and a substrate binding cleft. The inhibitor is useful for
CC the treatment and diagnosis of Alzheimer's disease. It is useful in
CC screens for individuals with a genetic predisposition to Alzheimer's
CC disease. The inhibitor is useful as a reagent for specifically binding to
CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
CC isolation, purification and characterisation.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
   ||||
Db 4 NIDA 7

RESULT 35
AAB61337
ID AAB61337 standard; peptide; 10 AA.
XX
AC AAB61337;
XX
XX 02-APR-2001 (first entry)
XX
XX Swedish mutation peptide from beta amyloid precursor protein.
XX
DE Memapsin 2; catalyst; Alzheimer's.
XX
XX Unidentified.
XX
XX WO200100663-A2.
XX
XX 04-JAN-2001.
XX
XX 27-JUN-2000; 2000WO-US17661.
XX
XX 28-JUN-1999; 99US-0141363.
XX 30-NOV-1999; 99US-0168060.
XX 25-JAN-2000; 2000US-0177836.
XX 27-JAN-2000; 2000US-0178368.
XX 08-JUN-2000; 2000US-0210292.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Tang JUN, Lin X, Koelsch G;
XX
XX WPI; 2001-102885/11.
XX
XX Purified recombinant catalytically active memapsin 2, used to screen
PT inhibitors of it, which are used to treat and prevent Alzheimer's
PT disease -
XX
XX Claim 6; Page 11; 86pp; English.
XX
XX The present invention relates to a purified recombinant
CC catalytically active memapsin 2. The invention may be used for
CC isolating inhibitors which are used to treat or prevent
CC Alzheimer's disease. The invention may also be used to screen
CC for individuals more genetically prone to develop Alzheimer's
XX disease.
XX

```

SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
1111
4 NIDA 7RESULT 36
AAU99491

ID AAU99491 standard; peptide: 10 AA.

AC AAU99491;

DT 07-OCT-2002 (first entry)

DE Peptide #2 used as substrate for human memapsin 2.

XX Human; memapsin 2; beta secretase; aspartic protease; APP;

KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;

KW neuroprotective; nootropic.

XX Homo sapiens.

OS Synthetic.

XX US2002049303-A1.

XX 25-APR-2002.

XX 28-FEB-2001; 2001US-0796264.

XX 28-JUN-1999; 99US-141363P.

XX 30-NOV-1999; 99US-168060P.

XX 25-JAN-2000; 2000US-178368P.

XX 27-JAN-2000; 2000US-178368P.

XX 27-JUN-2000; 2000US-0604608.

XX (TANG/) TANG J J N.

XX (LINX/) LIN X.

XX (KOEL/) KOELSCH G.

XX (HONG/) HONG L.

XX Tang JUN, Lin X, Koelsch G, Hong L;

XX WPI; 2002-507280/54.

XX New recombinant catalytically active memapsin 2, useful to screen for

XX inhibitors of memapsin 2 which can be used to prevent and treat

XX Alzheimer's disease

XX Claim 6; Page 30; 44pp; English.

XX The present invention relates to methods for the production of

XX purified, recombinant catalytically active, memapsin 2 (beta

XX secretase). Memapsin 2, a member of the aspartic protease family,

XX cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.

XX The recombinant memapsin 2 is useful for identifying inhibitors of

XX memapsin 2 in the design of drugs for the treatment and/or prevention

XX of Alzheimer's disease. The recombinant memapsin 2 can be used to

XX immunise against Alzheimer's disease. The present sequence represents

XX a peptide used as a substrate for human memapsin 2.

XX Sequence 10 AA;

Query Match 100.0%; Score 20; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
1111

DB 4 NIDA 7

RESULT 37
ABB78614

ID ABB78614 standard; peptide: 10 AA.

AC ABB78614;

DT 16-JUL-2002 (first entry)

DE Beta-secretase specific substrate PHA-247574E SEQ ID NO:63.

XX Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;

XX proteolytic.

XX Synthetic.

XX GB2367060-A.

XX 27-MAR-2002.

XX 29-OCT-2001; 2001GB-0025934.

XX 23-SEP-1999; 99US-155493P.

XX 23-SEP-1999; 99US-0404133.

XX 23-SEP-1999; 99WO-0520881.

XX 13-OCT-1999; 99US-0416901.

XX 06-DEC-1999; 99US-169232P.

XX 22-SEP-2000; 2000GB-0023315.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Bienkowski MJ, Gurney M;

XX WPI; 2002-396337/43.

XX Human aspartyl protease 1 substrates useful in assays to detect

XX aspartyl protease activity, e.g. for the diagnosis of Alzheimer's

XX disease

XX Example 15; Page 92; 182pp; English.

XX The present invention describes a human aspartyl protease 1 (hu-Asp1)

XX substrate (I) which comprises a peptide of no more than 50 amino acids,

XX and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-

XX Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1

XX proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with

XX (1) under acidic conditions; and (b) determining the level of hu-Asp1

XX proteolytic activity; (2) a purified polynucleotide (III) comprising a

XX nucleotide sequence that hybridises under stringent conditions to the

XX non-coding strand complementary to a defined 1804 nucleotide sequence

XX (see ABL2436) where the nucleotide sequence encodes a polypeptide having

XX Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane

XX domain); (3) a purified polynucleotide (III') comprising a sequence that

XX hybridises under stringent conditions to (III) (the nucleotide sequence

XX encodes a polypeptide further lacking a pro-peptide domain corresponding

XX to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)

XX comprising (III) or (III'); and (5) a host cell (V) transformed or

XX transfected with (III), (III') and/or (IV). The hu-Asp1 protease

XX substrate (I) may be used as an enzyme substrate in assays to detect

XX aspartyl protease activity, (II) and therefore diagnose diseases

XX associated with aberrant hu-Asp1 expression and activity such as

XX Alzheimer's disease. hu-Asp1 has been localised to chromosome 21, while

XX hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present

XX sequence represents a beta-secretase specific substrate peptide which is

XX used in an example from the present invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 20; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 4 NLDA 7

RESULT 38
 AAB06425 standard; Peptide; 10 AA.

ID AAB06425
 AC ABB06425;
 DT 31-MAY-2002 (first entry)
 DE Human APP Swedish KM-NL mutation beta-secretase cleavage sequence SEQ.19.
 KM Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KM aspartyl protease; neuroprotective; nontropic; beta-secretase inhibitor;
 KM Alzheimer's disease.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200206306-A2.
 PD 24-JAN-2002.
 PE 19-JUL-2001; 2001WO-US23035.
 XX 19-JUL-2000; 2000US-219795P.
 PR 12-MAR-2001; 2001US-275251P.
 XX (PHMA) PHARMACIA & UPJOHN CO.
 PA Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Helmlison RL;
 DR WPI; 2002-216995/27.
 XX Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease -
 PS Claim 19; Page 84; 188pp; English.

CC The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (1) has neuroprotective and
 CC nontropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (1) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (1) is useful
 CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.

SQ Sequence 10 AA;
 XX

Query Match 100.0%; Score 20; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 4 NLDA 7

RESULT 39
 AAB75142

ID AAB75142 standard; peptide; 11 AA.
 XX AAB75142;
 AC 08-AUG-2001 (first entry)
 DT APP Swedish variant sequence (from P6 to P5') peptide substrate SEQ.2.
 DE APP Swedish variant sequence (from P6 to P5') peptide substrate SEQ.2.
 KM Amyloid precursor protein; APP; Asp 1; endocapsin 1; inhibition;
 KM transmembrane aspartyl proteinase; APP Swedish variant; nontropic;
 KM neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
 KM beta amyloid protein-related disease; antialzheimer.
 OS Homo sapiens.
 PN WO200131054-A1.
 PD 03-MAY-2001.
 PF 19-OCT-2000; 2000WO-GB04028.
 PR 22-OCT-1999; 99GB-0025136.
 XX (SMIR) SMITHKLINE BEECHAM PLC.
 PA (SMIR) SMITHKLINE BEECHAM CORP.
 PI Christie G, Hussain I, Powell DJ;
 DR WPI; 2001-328654/34.
 XX Identifying inhibitors of Asp 1-mediated cleavage, for treating or
 PT preventing beta-amyloid protein-related disease, comprises measuring
 PT the extent of substrate cleavage in a reaction system containing Asp 1
 PT and a substrate -
 PS Claim 3; Page 24; 31pp; English.

CC The present invention describes a method of screening for compounds
 CC which inhibit Asp 1-mediated cleavage of a polypeptide or protein
 CC substrate. The method comprises providing a reaction system comprising
 CC Asp 1 and substrate, and measuring the extent of cleavage of the
 CC substrate in the presence of test compound compared with that in the
 CC presence of the test compound. Also described are: (1) a method of
 CC screening for compounds which inhibit Asp 1 mediated cleavage of a
 CC polypeptide or protein substrate comprising providing a reaction system
 CC comprising Asp 1 and a labeled active site ligand, and measuring the
 CC extent of binding of the labeled ligand in the presence of test compound
 CC compared with that in the presence of the test compound; (2) a compound
 CC identified by the method; (3) a pharmaceutical composition comprising the
 CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 modulated
 CC amyloid precursor protein (APP) cleavage, or treating or prophylaxis of
 CC beta-amyloid protein-related disease, comprising administering to a
 CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1
 CC modulated APP cleavage; and (6) a method for treating or prophylaxis of
 CC beta-amyloid protein-related disease comprising administering a compound
 CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a
 CC polypeptide or protein is useful in therapy, in the preparation of a
 CC medicament for inhibiting Asp 1-modulated APP cleavage and for the
 CC treatment or prophylaxis of beta-amyloid protein-related disease, APP
 CC including Alzheimer's disease. The present sequence represents an APP
 CC Swedish variant sequence (from P6 to P5') peptide substrate, which can
 CC be used in the method of the invention.

SQ Sequence 11 AA;
 XX

Query Match 100.0%; Score 20; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 5 NLDA 8

RESULT 40
AAB75145
ID AAB75145 standard; peptide: 11 AA.
XX
AC AAB75145;
XX
DT 08-AUG-2001 (first entry)
XX
DE Asp 1 substrate sequence SEQ ID NO:4.
XX
XX Amyloid precursor protein; Asp 1; endorepsin 1; inhibition;
KM transmembrane aspartyl proteinase; Asp Swedish variant; nototropic;
KM neuroprotective; beta-secretase cleavage site; Alzheimer's disease;
KM beta amyloid protein-related disease; antiAlzheimer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminally attached to maltose binding protein
FT (MBP)"
FT
FT
PN WO200131054-A1.
PN
PD 03-MAY-2001.
XX
XX 19-OCT-2000; 2000WO-GB04028.
XX
XX 22-OCT-1999; 99GB-0025136.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Christie G, Hussain I, Powell DJ;
XX
XX WPI: 2001-328654/34.
XX
XX Identifying inhibitors of Asp 1-mediated cleavage, for treating or
PT preventing beta-amyloid protein-related disease, comprises measuring
PT the extent of substrate cleavage in a reaction system containing Asp 1
PT and a substrate -
XX
PS Disclosure: Page 3; 31pp; English.
XX
XX The present invention describes a method of screening for compounds
CC which inhibit Asp 1-mediated cleavage of a polypeptide or protein
CC substrate. The method comprises providing a reaction system comprising
CC Asp 1 and substrate, and measuring the extent of cleavage of the
CC substrate in the presence of test compound compared with that in the
CC presence of the test compound. Also described are: (1) a method of
CC screening for compounds which inhibit Asp 1 mediated cleavage of a
CC polypeptide or protein substrate comprising providing a reaction system
CC comprising Asp 1 and a labeled active site ligand, and measuring the
CC extent of binding of the labeled ligand in the presence of test compound
CC compared with that in the presence of the test compound; (2) a compound
CC identified by the method; (3) a pharmaceutical composition comprising the
CC compound of (2) and a carrier; (4) a method of inhibiting Asp 1 mediated
CC beta-amyloid precursor protein (APP) cleavage, or treating or prophylaxis of
CC beta-amyloid protein-related disease, comprising administering to a
CC patient a compound of (2); (5) a compound which is an inhibitor of Asp 1
CC mediated APP cleavage; and (6) a method for treating or prophylaxis of
CC beta-amyloid protein-related disease comprising administering a compound
CC of (2) or (5). The compound which inhibits Asp 1 mediated cleavage of a
CC polypeptide or protein is useful in therapy, in the preparation of a
CC medicament for inhibiting Asp 1-mediated APP cleavage and for the
CC treatment or prophylaxis of beta-amyloid protein-related disease, an
CC including Alzheimer's disease. The present sequence represents an Asp 1
CC substrate sequence which is given in the exemplification of the present
XX invention.
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 20; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Asp2 substrate Swedish variant peptide sequence.
XX
XX Asp2; endorepsin 2; memapsin 2; beta-amyloid protein;
KM Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;
KM Asp2 inhibitor.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT
FT
PN WO200129563-A1.
PN
PD 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-GB04039.
XX
XX 21-OCT-1999; 99GB-0024957.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Christie G, Hussain I, Powell DJ;
XX
XX WPI: 2001-300381/31.
XX
XX Screening for inhibitors of Asp 2 mediated polypeptide cleavage
PT comprises measuring substrate cleavage or ligand binding with a system
PT comprising Asp 2 and a substrate or labelled ligand in the presence or
PT absence of a test compound -
XX
PS Claim 3; Page 26; 34pp; English.
XX
XX The present invention describes a method of screening for compounds which
CC inhibit Asp2 (also known as memapsin 2 and endorepsin 2) mediated
CC cleavage of a protein substrate, involving measuring the extent of
CC cleavage of the substrate in the presence and absence of the test
CC compound. Asp2 is thought to be involved in the cleavage of amyloid
CC precursor protein which is excised to produce beta-amyloid. Beta-amyloid
CC is involved in the pathogenesis of Alzheimer's disease, Parkinson's
CC disease, cortical Lewy body disease and vascular and cerebrovascular
CC diseases, and Asp2 inhibitors could be useful in their treatment. The
CC present sequence is an example of an Asp2 substrate.
XX
SQ Sequence 11 AA;
XX
XX Query Match 100.0%; Score 20; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 1e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 NIDA 4
XX |||||
XX Db 5 NIDA 8


```

RESULT 42
AAM52699
ID AAM52699 standard; peptide: 11 AA.
XX
AC AAM52699;
XX
DT 26-FEB-2002 (first entry)
XX
DE Beta-secretase substrate peptide.
XX
KW Beta-secretase substrate; inhibitor; amine compound;
KW beta amyloid protein production; head injury; spinal injury;
KW amyloid precursor protein alpha secretion; nerve damage;
KW meningitis sequelae; cerebral paralysis; memory disorder;
KW mental disease; nootropic; neuroprotective; cerebroprotective.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Nma-Ser"
FT Modified-site 9 /note= "Lys(Dnp)"
FT Modified-site 11 /note= "C-terminal amide"
XX
XX WO200187293-A1.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP04144.
XX
PR 19-MAY-2000; 2000JP-0152758.
XX
PA (TAKEDA ) TAKEDA CHEM IND LTD.
XX
PI Miyamoto M, Matsui J, Fukumoto H, Tarui N;
XX
DR WPI; 2002-055640/07.
XX
PT Beta-secretase inhibitor used for treating e.g. Alzheimer's disease and
PT injury to brain or spine, and neurodegeneration, comprises amine
PT compound -
XX
PS Examples; Page 66; 86pp; Japanese.
XX
CC The invention relates to novel amine compounds which are beta-secretase
CC inhibitors. The beta-secretase compounds also have the ability to
CC promote amyloid precursor protein alpha secretion and to inhibit beta
CC amyloid protein production. The beta-secretase inhibitors of the
CC invention can be used for treating head or spinal injuries, nerve damage,
CC sequelae of meningitis, cerebral paralysis, memory disorders and mental
CC diseases. The present sequence represents a beta-secretase substrate
CC peptide used in the exemplifications of the invention.
XX
SQ Sequence 11 AA;
XX
QY Query Match 100.0%; Score 20; DB 23; Length 11;
DB Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 NLDA 4
DB 4 NLDA 7
XX
RESULT 43
ABB08996
ID ABB08996 standard; peptide: 12 AA.
XX
AC ABB08996;
XX

```

```

DT 19-JUN-2002 (first entry)
XX
DE Amyloid precursor protein substrate #1.
XX
KW Amyloid precursor protein; APP; Alzheimer's disease; nootropic;
KW neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;
KW Down's syndrome; cerebral amyloid angiopathy; dementia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal biotin"
FT Modified-site 10 /note= "Oregon green covalently linked"
XX
XX WO200202505-A2.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US20852.
XX
PR 30-JUN-2000; 2000US-215323P.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Fang LY, Hom R, John V, Malliaind M;
XX
DR WPI; 2002-171625/22.
XX
PT New substituted amines are e.g. beta-amyloid peptide inhibitors, useful
PT for treating Alzheimer's disease, mild cognitive impairment and Down's
PT syndrome -
XX
PS Example B; Page 94; 136pp; English.
XX
CC This invention relates to substituted amines and their salts, which
CC are nootropic, neuroprotective, cerebroprotective, haemostatic and
CC antiparkinsonian in their action. They are used in the preparation of
CC a composition useful for treating, preventing or delaying the on-set
CC of Alzheimer's disease, for treating mild cognitive impairment, Down's
CC syndrome, cerebral amyloid angiopathy, dementia associated with
CC Parkinson's disease, dementia associated with progressive supranuclear
CC palsy, and dementia associated with cortical basal degeneration.
CC They are also useful for treating diseases characterised by beta-amyloid
CC deposits in brain, and for producing beta-secretase complexes. This
CC sequence represents an amyloid precursor protein substrate that can be
CC cleaved by beta secretase. This substrate is used to assay
CC beta-secretase activity.
XX
SQ Sequence 12 AA;
XX
QY Query Match 100.0%; Score 20; DB 23; Length 12;
DB Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 NLDA 4
DB 4 NLDA 7
XX
RESULT 44
ABB07591
ID ABB07591 standard; peptide: 12 AA.
XX
AC ABB07591;
XX
DT 08-MAY-2002 (first entry)
XX
DE Biotinylated synthetic APP substrate.
XX
KW APP; amine derivative; beta-secretase; amyloid precursor protein; A beta;
KW amyloid beta peptide; beta-amyloid; nootropic; neuroprotective;

```

```

KW cerebroprotective; haemostatic; antiparkinsonian.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "N-terminal blotin"
FT Region 10..11
FT /note= "covalent attachment of oregon green"
XX
XX WO200202520-A2.
XX
XX 10-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-US21000.
XX
XX 30-JUN-2000; 2000US-215323P.
XX
XX 29-JUN-2001; 2001US-0895843.
XX
XX (ELAN-) ELAN PHARM INC.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Beck JP, Gallunas A, Hom R, Jagodzinska B, John V, Maillard M;
XX WPI; 2002-188416/24.
XX
XX New disubstituted amine derivatives, useful for treating Alzheimer's
XX disease and other degenerative diseases -
XX
XX Example B; Page 160; 286pp; English.
XX
XX The invention relates to disubstituted amine derivatives of specified
XX formulae or their salts. The amine derivatives can inhibit beta-secretase
XX activity or inhibit the cleavage of amyloid precursor protein (APP) in a
XX reaction mixture. They can also be used to inhibit production of amyloid
XX beta peptide (A beta) in a cell or inhibit production of beta-amyloid
XX plaque in an animal. The amine derivatives are useful for treating or
XX preventing a disease characterized by beta-amyloid deposits in the brain
XX e.g. for treating or preventing Alzheimer's disease (AD), for helping
XX prevent or delay the onset of AD, for treating mild cognitive impairment
XX (MCI), preventing or delaying the onset of AD in those who would progress
XX from MCI to AD, for treating Down's syndrome, humans who have hereditary
XX cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
XX amyloid angiopathy and preventing its potential consequences i.e. single
XX and recurrent lobar haemorrhages, for treating other degenerative
XX diseases, including dementias of mixed vascular and degenerative origin,
XX dementia associated with parkinson's disease, dementia associated with
XX progressive supranuclear palsy, dementia associated with cortical basal
XX degeneration, diffuse lewy body type of Alzheimer's disease. Sequences
XX ABB07591-595 are synthetic APP substrates that can be cleaved by beta-
XX secretase and are used to assay beta-secretase activity in the presence
XX or the absence of the inhibitory compounds of the invention.
XX
XX Sequence 12 AA:
SQ
Query Match 100.0%; Score 20; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
XX | | | |
XX 4 NIDA 7
Db

```

RESULT 45
AAE16656 standard; peptide; 12 AA.

AAE16656;

09-APR-2002 (first entry)

APP substrate peptide #1 used in cell free inhibition assay.

```

XX Disubstituted amine derivative; Alzheimer's disease; Down's syndrome;
KW degenerative disease; beta-amyloid deposit; mild cognitive impairment;
KW hereditary cerebral haemorrhage; amyloidosis; degenerative dementia;
KW cerebral amyloid angiopathy; parkinson's disease; supranuclear palsy;
KW cortical basal degeneration; AD; MCI; amyloid precursor protein;
KW APP substrate; beta-secretase; amyloid beta peptide; A beta peptide.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "Biotin labelled"
FT Modified-site 10
FT /note= "Oregon green labelled Arg"
XX
XX WO200202518-A2.
XX
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US20856.
XX
XX 30-JUN-2000; 2000US-215323P.
XX
XX (ELAN-) ELAN PHARM INC.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Beck JP, Gallunas A, Hom R, Jagodzinska B, John V, Maillard M;
XX WPI; 2002-122550/16.
XX
XX New disubstituted amine derivatives, useful for treating Alzheimer's
XX disease and other degenerative diseases -
XX
XX Example B; Page 160; 286pp; English.
XX
XX The invention relates to disubstituted amine derivative compounds
XX useful for treating Alzheimer's disease and other degenerative diseases.
XX Compounds of the invention possess beta secretase inhibitory activity and
XX are useful for inhibiting beta-secretase mediated cleavage of amyloid
XX precursor protein (APP) and particularly, to inhibit the production of
XX amyloid beta (A beta) peptide. They are useful for treating or preventing
XX a disease characterised by beta-amyloid deposits in the brain e.g. for
XX treating or preventing Alzheimer's disease (AD), for helping to prevent
XX or delay the onset of Alzheimer's disease, for treating mild cognitive
XX impairment (MCI), Down's syndrome, hereditary cerebral angiopathy and
XX the amyloidosis of the Dutch type, cerebral amyloid angiopathy with
XX preventing its potential consequences i.e. single and recurrent lobar
XX haemorrhages, for treating other degenerative dementias including
XX dementias of mixed vascular and degenerative origin, dementia associated
XX with Parkinson's disease, dementia associated with progressive
XX supranuclear palsy, dementia associated with cortical basal degeneration
XX and diffuse lewy body type of Alzheimer's disease. The present sequence
XX is APP substrate used to assay beta-secretase activity in the presence
XX or absence of inhibitory compounds of the invention.
XX
XX Sequence 12 AA:
SQ
Query Match 100.0%; Score 20; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
XX | | | |
XX 4 NIDA 7
Db

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Search completed: February 6, 2003, 11:19:42
Job time : 28.8333 secs

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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 ; Search time 9.33333 Seconds
(Without alignments)
12.610 Million cell updates/sec

Title: PAT943-6
Perfect score: 20
Sequence: 1 nlda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 561

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	4	US-09-548-372D-66	Sequence 66, Appl
2	20	100.0	4	US-09-548-367D-66	Sequence 66, Appl
3	20	100.0	5	US-08-480-498-2	Sequence 2, Appl
4	20	100.0	5	US-08-659-984A-14	Sequence 14, Appl
5	20	100.0	5	US-08-660-531-14	Sequence 14, Appl
6	20	100.0	5	US-09-054-334-2	Sequence 2, Appl
7	20	100.0	9	US-08-802-981-219	Sequence 219, Appl
8	20	100.0	10	US-08-659-984A-19	Sequence 19, Appl
9	20	100.0	10	US-08-660-531-19	Sequence 19, Appl
10	20	100.0	10	US-09-548-372D-63	Sequence 63, Appl
11	20	100.0	10	US-09-548-367D-63	Sequence 63, Appl
12	20	100.0	11	PCT-US94-07043A-3	Sequence 3, Appl
13	20	100.0	19	US-09-376-330-12	Sequence 12, Appl
14	20	100.0	21	US-08-659-984A-18	Sequence 18, Appl
15	20	100.0	21	US-08-802-981-112	Sequence 112, Appl
16	20	100.0	21	US-08-660-531-18	Sequence 18, Appl
17	20	100.0	30	US-08-659-984A-17	Sequence 17, Appl
18	20	100.0	30	US-08-433-522A-17	Sequence 17, Appl
19	20	100.0	30	US-09-135-166-17	Sequence 17, Appl
20	20	100.0	30	US-08-660-531-17	Sequence 17, Appl
21	20	100.0	30	US-08-942-046-17	Sequence 17, Appl
22	20	100.0	33	US-08-438-753B-18	Sequence 18, Appl
23	20	100.0	33	US-08-443-883A-18	Sequence 18, Appl
24	20	100.0	33	US-08-651-328-18	Sequence 18, Appl
25	20	100.0	33	US-08-455-524B-18	Sequence 18, Appl
26	20	100.0	33	US-08-659-984A-16	Sequence 16, Appl
27	20	100.0	33	US-08-455-021B-18	Sequence 18, Appl

28	20	100.0	33	4	US-09-045-467-18	Sequence 18, Appl
29	20	100.0	33	4	US-08-660-531-16	Sequence 16, Appl
30	20	100.0	42	2	US-08-659-984A-15	Sequence 15, Appl
31	20	100.0	42	4	US-08-660-531-15	Sequence 15, Appl
32	20	100.0	44	4	US-08-905-223-345	Sequence 345, Appl
33	20	100.0	46	3	US-08-924-330A-10	Sequence 10, Appl
34	20	100.0	46	4	US-09-138-721-10	Sequence 10, Appl
35	20	100.0	57	1	US-08-370-225-29	Sequence 29, Appl
36	20	100.0	57	1	US-08-370-225-30	Sequence 30, Appl
37	20	100.0	57	1	US-08-461-859-29	Sequence 29, Appl
38	20	100.0	57	1	US-08-461-859-30	Sequence 30, Appl
39	20	100.0	57	5	PCT-US93-10069-29	Sequence 29, Appl
40	20	100.0	57	5	PCT-US93-10069-30	Sequence 30, Appl
41	20	100.0	62	3	US-08-995-156A-40	Sequence 40, Appl
42	20	100.0	62	4	US-09-419-281-40	Sequence 40, Appl
43	20	100.0	63	3	US-08-995-156A-41	Sequence 41, Appl
44	20	100.0	63	3	US-08-995-156A-86	Sequence 86, Appl
45	20	100.0	63	4	US-09-419-281-41	Sequence 41, Appl

ALIGNMENTS

```

RESULT 1
US-09-548-372D-66
; Sequence 66, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-66
Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLDA 4
Db 1 NLDA 4
RESULT 2
US-09-548-367D-66
; Sequence 66, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493

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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 66
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-548-367D-66

Query Match 100.0%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
| | | |
DB 1 NIDA 4

RESULT 3
US-08-480-498-2
Sequence 2, Application US/08480498
Patent No. 5744346
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,498
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 015270-002200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-498-2

Query Match 100.0%; Score 20; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
| | | |
DB 2 NIDA 5

RESULT 4
US-08-659-984A-14
Sequence 14, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-00281005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-659-984A-14

Query Match 100.0%; Score 20; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
| | | |
DB 2 NIDA 5

RESULT 5
US-08-660-531-14
Sequence 14, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-531-14

Query Match 100.0%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 2 NLDA 5

RESULT 6
US-09-054-334-2
Sequence No. 6329163
Patent No. 6329163
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Jacobson-Croak, Kirsten L.
APPLICANT: Sinha, Sukanto
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,334
FILING DATE: 02-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 015270-002820US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-054-334-2

Query Match 100.0%; Score 20; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 2 NLDA 5

RESULT 7
US-08-802-981-219
Sequence 219, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-802-981-219

Query Match 100.0%; Score 20; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 4 NLDA 7

RESULT 8
US-08-659-984A-19
; Sequence 19, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-00281005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note="N-terminal Ser is acetylated."
US-08-659-984A-19
; Query Match 100.0%; Score 20; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
Db 4 NIDA 7
RESULT 9
US-08-660-531-19
; Sequence 19, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-00221005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note="N-terminal Ser is acetylated."
US-08-660-531-19
; Query Match 100.0%; Score 20; DB 4; Length 10;
; Best Local Similarity 100.0%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
Db 4 NIDA 7
RESULT 10
US-09-548-372D-63
; Sequence 63, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: 2000-04-12
; PRIOR APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

OTHER INFORMATION: Synthetic peptide
US-09-548-372D-63

Query Match 100.0%; Score 20; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 4 NLDA 7

RESULT 11
US-09-548-367D-63

Sequence 63, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
FILE REFERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-548-367D-63

Query Match 100.0%; Score 20; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 4 NLDA 7

RESULT 12
PCT-US94-07043A-3

Sequence 3, Application PC/US9407043A
GENERAL INFORMATION:
APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDGENIC
TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: Sharp PC 4600
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07043A

FILING DATE: June 21, 1994

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10889
FILING DATE: November 12, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/995,660
FILING DATE: December 16, 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880,914
FILING DATE: May 11, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Pamela A. Simonton
REGISTRATION NUMBER: 31,060

REFERENCE/DOCKET NUMBER: MTI 224.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 937-2340
TELEFAX: (203) 937-2795

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear

PCT-US94-07043A-3
Query Match 100.0%; Score 20; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 5 NLDA 8

RESULT 13
US-09-376-330-12

Sequence 12, Application US/09376330
Patent No. 6399321
GENERAL INFORMATION:
APPLICANT: Tessier, Daniel C.
APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
FILE REFERENCE: 2139-9"US"
CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 19
TYPE: PRT
ORGANISM: Mutant Q1429A RUGT
US-09-376-330-12

Query Match 100.0%; Score 20; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 8 NLDA 11

RESULT 14
US-08-659-984A-18

Sequence 18, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto

APPLICANT: Jacobson-Croak, Kirsten L.
 TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Ctr., 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659,984A
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,152
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-002810US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-659-984A-18

Query Match 100.0%; Score 20; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
 DB 4 NIDA 7

RESULT 15
 US-08-802-981-112
 ; Sequence 112, Application US/08802981
 ; Patent No. 6037137
 ; GENERAL INFORMATION:
 ; APPLICANT: Komoriya, Akira
 ; APPLICANT: Packard, Beverly S.
 ; TITLE OF INVENTION: Compositions for the Detection of Enzyme
 ; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
 ; NUMBER OF SEQUENCES: 231
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/802,981
 ; FILING DATE: 20-FEB-1997

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 016865-000300US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 112:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3
 OTHER INFORMATION: /product= "Alb"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /product= "Acp"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 16
 OTHER INFORMATION: /product= "Acp"
 US-08-802-981-112

Query Match 100.0%; Score 20; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
 DB 9 NIDA 12

RESULT 16
 US-08-660-531-18
 ; Sequence 18, Application US/08660531
 ; Patent No. 6221645
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,531
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,498
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-531-18

Query Match 100.0%; Score 20; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
||||
Db 4 NIDA 7

RESULT 17
US-08-659-984A-17
Sequence 17, Application US/0865984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-659-984A-17

Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NIDA 4
||||
Db 25 NIDA 28

RESULT 18
US-08-433-522A-17
Sequence 17, Application US/08433522A
Patent No. 6013514
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH FLOOR, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MTS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-433-522A-17

Query Match 100.0%; Score 20; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
||||
Db 19 NIDA 22

RESULT 19
US-09-135-166-17
Sequence 17, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH FLOOR, 330 University Avenue
CITY: Toronto
STATE: Ontario

```

: COUNTRY: Canada
: ZIP: M5G 1R7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/135,166
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/433,522
: FILING DATE: 12-SEP-1995
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: STEWART, Michael I
: REGISTRATION NUMBER: 24,973
: REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 595-1155
: TELEFAX: (416) 595-1163
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-135-166-17

Query Match          100.0%; Score 20; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
   ||||
Db 19 NIDA 22

RESULT 20
: US-08-660-531-17
: Sequence 17, Application US/08660531
: Patent No. 6221645
: GENERAL INFORMATION:
: APPLICANT: Chrysler, Susanna M.S.
: APPLICANT: Simha, Sukanto
: APPLICANT: Kelm, Pamela S.
: APPLICANT: Anderson, John P.
: TITLE OF INVENTION: Beta-Secretase
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Ctr., 8th Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/660,531
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/480,498
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Heslin, James W.
: REGISTRATION NUMBER: 29,541
: REFERENCE/DOCKET NUMBER: 15270-002210US

```

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: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-660-531-17

Query Match          100.0%; Score 20; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
   ||||
Db 25 NIDA 28

RESULT 21
: US-08-942-046-17
: Sequence 17, Application US/08942046
: Patent No. 6264954
: GENERAL INFORMATION:
: APPLICANT: CHONG, Pele
: APPLICANT: THOMAS, Wayne
: APPLICANT: YANG, Yan Ping
: APPLICANT: LOOSMORE, Sheena
: APPLICANT: SIA, Dwo Yuan Charles
: APPLICANT: KLEIN, Michel
: TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
: NUMBER OF SEQUENCES: 55
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sim & McBurney
: STREET: 6TH Floor, 330 University Avenue
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5G 1R7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/942,046
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/433,522
: FILING DATE: 12-SEP-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: STEWART, Michael I
: REGISTRATION NUMBER: 24,973
: REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 595-1155
: TELEFAX: (416) 595-1163
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-942-046-17

Query Match          100.0%; Score 20; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NLDA 4
DB 19 NLDA 22

RESULT 22
US-08-438-753B-18

; Sequence 18, Application US/08438753B
; Patent No. 5705363

; GENERAL INFORMATION:

; APPLICANT: Imakawa, Kazuhito

; TITLE OF INVENTION: Interferon Tau Compositions and

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/438,753B

; FILING DATE: 10-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/139,891

; FILING DATE: 19-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/847,741

; FILING DATE: 09-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/318,050

; FILING DATE: 02-MAR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/969,890

; FILING DATE: 30-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615

; REFERENCE/DOCKET NUMBER: 5600-0001.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-324-0880

; TELEFAX: 415-324-0960

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: Amino acid sequence of fragment

; INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4

US-08-438-753B-18

Query Match 100.0%; Score 20; DB 1; Length 33;
Best local Similarity 100.0%; Pred. NO. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
DB 6 NLDA 9

RESULT 23

US-08-443-883A-18

; Sequence 18, Application US/08443883A

; Patent No. 5738845

; GENERAL INFORMATION:

; APPLICANT: Bazer, Fuller W.

; APPLICANT: Johnson, Howard M.

; APPLICANT: Pontzer, Carol H.

; APPLICANT: Ott, Troy L.

; APPLICANT: Van Heeke, Gino

; APPLICANT: Imakawa, Kazuhito

; TITLE OF INVENTION: Interferon Tau Compositions and

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/443,883A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/139,891

; FILING DATE: 19-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/847,741

; FILING DATE: 09-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/318,050

; FILING DATE: 02-MAR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/969,890

; FILING DATE: 30-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fabian, Gary R.

; REGISTRATION NUMBER: 33,875

; REFERENCE/DOCKET NUMBER: 5600-0001.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-324-0880

; TELEFAX: 415-324-0960

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: Amino acid sequence of fragment

; INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4

US-08-443-883A-18

Query Match 100.0%; Score 20; DB 1; Length 33;
Best local Similarity 100.0%; Pred. NO. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
DB 6 NLDA 9

RESULT 24

US-08-631-328-18

; Sequence 18, Application US/08631328

; Patent No. 5939286

; GENERAL INFORMATION:

; APPLICANT: Johnson, Howard M.

APPLICANT: Pontzer, Carol H.
APPLICANT: Subramaniam, Prem S.
TITLE OF INVENTION: Hybrid Interferon Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,328
FILING DATE: 12-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-08-631-328-18
Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
DB 6 NIDA 9
RESULT 25
US-08-455-524B-18
Sequence 18, Application US/08455524B
Patent No. 5942223
GENERAL INFORMATION:
APPLICANT: Bazer, Fuller W.
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Ott, Troy L.
APPLICANT: Van Heeke, Gino
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,524B
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-08-455-524B-18
Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
DB 6 NIDA 9
RESULT 26
US-08-659-984A-16
Sequence 16, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Pontzer, Carol H.
APPLICANT: Subramaniam, Prem S.
TITLE OF INVENTION: Hybrid Interferon Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,328
FILING DATE: 12-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-08-631-328-18
Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
DB 6 NIDA 9
RESULT 25
US-08-455-524B-18
Sequence 18, Application US/08455524B
Patent No. 5942223
GENERAL INFORMATION:
APPLICANT: Bazer, Fuller W.
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Ott, Troy L.
APPLICANT: Van Heeke, Gino
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,524B
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-08-455-524B-18
Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
DB 6 NIDA 9
RESULT 26
US-08-659-984A-16
Sequence 16, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Pontzer, Carol H.
APPLICANT: Subramaniam, Prem S.
TITLE OF INVENTION: Hybrid Interferon Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,328
FILING DATE: 12-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-08-631-328-18
Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
DB 6 NIDA 9
RESULT 25
US-08-455-524B-18
Sequence 18, Application US/08455524B
Patent No. 5942223
GENERAL INFORMATION:
APPLICANT: Bazer, Fuller W.
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Ott, Troy L.
APPLICANT: Van Heeke, Gino
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,524B
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-08-455-524B-18
Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
DB 6 NIDA 9
RESULT 26
US-08-659-984A-16
Sequence 16, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-00281005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-659-984A-16

Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
Db 16 NLDA 19

RESULT 27
US-08-455-021B-18
Sequence 18, Application US/08455021B
GENERAL INFORMATION:
APPLICANT: Bazer, Fuller W.
APPLICANT: Johnson, Howard W.
APPLICANT: Fontzer, Carol H.
APPLICANT: Olt, Troy L.
APPLICANT: Van Heeke, Gino
APPLICANT: Imakawa, Kazuhiko
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,021B
FILING DATE: 31-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890

FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 5600-0001.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-08-455-021B-18

Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
Db 6 NLDA 9

RESULT 28
US-09-045-467-18
Sequence 18, Application US/09045467
GENERAL INFORMATION:
APPLICANT: Johnson, Howard W.
APPLICANT: Pontzer, Carol H.
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,467
FILING DATE: 20-MAR-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/455,021
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 5600-0001.36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880

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;
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 33 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
;   INDIVIDUAL ISOLATE: Amino acid sequence of fragment
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-045-467-18
;
Query Match          100.0%; Score 20; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NIDA 4
      ||||
Db       6 NIDA 9

RESULT 29
US-08-660-531-16
; Sequence 16, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
;   APPLICANT: Chrysler, Susanna M.S.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Keim, Pamela S.
;   APPLICANT: Anderson, John P.
;   TITLE OF INVENTION: Beta-Secretase
;   NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Ctr., 8th Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/660,531
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/480,498
;   FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Heslin, James M.
;   REGISTRATION NUMBER: 29,541
;   REFERENCE/DOCKET NUMBER: 15270-0022100S
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-326-2400
;   TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 33 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-16

Query Match          100.0%; Score 20; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 NIDA 4
      ||||
Db       16 NIDA 19

RESULT 30
US-08-659-984A-15
; Sequence 15, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
;   APPLICANT: Anderson, John P.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Jacobson-Croak, Kirsten L.
;   TITLE OF INVENTION: Assays for Detecting Beta-Secretase
;   NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Ctr., 8th Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/659,984A
;   FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/485,152
;   FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Heslin, James M.
;   REGISTRATION NUMBER: 29,541
;   REFERENCE/DOCKET NUMBER: 15270-0028100S
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-326-2422
;   TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 42 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-15

Query Match          100.0%; Score 20; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NIDA 4
      ||||
Db       25 NIDA 28

RESULT 31
US-08-660-531-15
; Sequence 15, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
;   APPLICANT: Chrysler, Susanna M.S.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Keim, Pamela S.
;   APPLICANT: Anderson, John P.
;   TITLE OF INVENTION: Beta-Secretase
;   NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
```

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-531-15

Query Match 100.0%; Score 20; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
DB 25 NLDA 28

RESULT 32
US-08-905-223-345
Sequence 345, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 345:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: sig-peptide
LOCATION: -18..-1
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 4.8
OTHER INFORMATION: seq LEA1SSLSFVLG/RM
US-08-905-223-345

Query Match 100.0%; Score 20; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
DB 30 NLDA 33

RESULT 33
US-08-924-330A-10
Sequence 10, Application US/08924330A
Patent No. 6022948
GENERAL INFORMATION:
APPLICANT: Goldberg, Gregory I.
TITLE OF INVENTION: Method of Cell Surface Activation
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer
STREET: 800 No. 6022948th Lindbergh Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,330A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026,226
FILING DATE: 17-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: WU-2982
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-694-3117
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 46
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-330A-10

Query Match 100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
|||
Db 2 NIDA 5

RESULT 34
US-09-138-721-10
; Sequence 10, Application US/09138721
; Patent No. 6274703

GENERAL INFORMATION:

APPLICANT: Goldberg, Gregory I.

TITLE OF INVENTION: Method of Cell Surface Activation

TITLE OF INVENTION: and Inhibition

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scott J. Meyer

STREET: 800 No. 6274703th Lindbergh Blvd.

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/138,721

FILING DATE: 24-AUG-1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/942,330

FILING DATE: 5-SEPT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Meyer, Scott J.

REGISTRATION NUMBER: 25,275

REFERENCE/DOCKET NUMBER: WU-2982/2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-694-3117

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 46

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-138-721-10

Query Match 100.0%; Score 20; DB 4; Length 46;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
|||
Db 2 NIDA 5

RESULT 35
US-08-370-225-29

; Sequence 29, Application US/08370225

; Patent No. 5580736

GENERAL INFORMATION:

APPLICANT: Brent, Roger

APPLICANT: Gyuris, Jeno

APPLICANT: Golemis, Erica

TITLE OF INVENTION: Interaction Trap System for Isolating

TITLE OF INVENTION: No. 5580736el Proteins

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 555x

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,225

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,038

FILING DATE: 10/30/92

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/143001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 57

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-370-225-29

Query Match 100.0%; Score 20; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
|||
Db 15 NIDA 18

RESULT 36
US-08-370-225-30

; Sequence 30, Application US/08370225

; Patent No. 5580736

GENERAL INFORMATION:

APPLICANT: Brent, Roger

APPLICANT: Gyuris, Jeno

APPLICANT: Golemis, Erica

TITLE OF INVENTION: Interaction Trap System for Isolating

TITLE OF INVENTION: No. 5580736el Proteins

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 555x

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,225

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,038

FILING DATE: 10/30/92

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/143001

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-370-225-30

Query Match 100.0%; Score 20; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 15 NLDA 18

RESULT 37
US-08-461-859-29
Sequence 29, Application US/08461859
Patent No. 5786169
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
NUMBER OF INVENTION: No. 5786169el Proteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,859
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/143002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-461-859-29

Query Match 100.0%; Score 20; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 15 NLDA 18

RESULT 38
US-08-461-859-30
Sequence 30, Application US/08461859
Patent No. 5786169
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
NUMBER OF INVENTION: No. 5786169el Proteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,859
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/143002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-461-859-30

Query Match 100.0%; Score 20; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 15 NLDA 18

RESULT 39
PCT-US93-10069-29
Sequence 29, Application PC/TUS9310069
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
NUMBER OF INVENTION: Novel Proteins

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10069
FILING DATE: 20-OCT-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/143001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-10069-29

Query Match 100.0%; Score 20; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
1111
DB 15 NLDA 18

RESULT 40
PCT-US93-10069-30
Sequence 30, Application PC/TUS9310069
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: Novel Proteins
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10069
FILING DATE: 20-OCT-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038

FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/143001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-10069-30

Query Match 100.0%; Score 20; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
1111
DB 15 NLDA 18

RESULT 41
US-08-995-156A-40
Sequence 40, Application US/08995156A
Patent No. 6028169
GENERAL INFORMATION:
APPLICANT: KREIDER, BRENT L.
APPLICANT: RUBEN, STEVEN M.
APPLICANT: OLSEN, HENRIK S.
TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0; Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,156A
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/042,269
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-156A-40

Query Match 100.0%; Score 20; DB 3; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 42

US-09-419-281-40
; Sequence 40, Application US/09419281
; Patent No. 6379926

GENERAL INFORMATION:

APPLICANT: KREIDER, BRENT L.
RUBEN, STEVEN M.
OLSEN, HENRIK S.

TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/419,281

FILING DATE: 15-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: 08/995,156

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0340004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 62 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-419-281-40

Query Match 100.0%; Score 20; DB 4; Length 62;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 43

US-08-995-156A-41

; Sequence 41, Application US/08995156A

; Patent No. 6028169

GENERAL INFORMATION:

APPLICANT: KREIDER, BRENT L.
RUBEN, STEVEN M.
OLSEN, HENRIK S.

TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/995,156A

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/042,269

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0340004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 63 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-995-156A-41

Query Match 100.0%; Score 20; DB 3; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 44

US-08-995-156A-86

; Sequence 86, Application US/08995156A

; Patent No. 6028169

GENERAL INFORMATION:

APPLICANT: KREIDER, BRENT L.
RUBEN, STEVEN M.
OLSEN, HENRIK S.

TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/995,156A

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/042,269

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0340004

Search completed: February 6, 2003, 11:24:10
 Job time : 10.333 secs

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 63 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-995-156A-86

Query Match 100.0%; Score 20; DB 3; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
 ||||
 Db 60 NLDA 63

RESULT 45

US-09-419-281-41
 ; Sequence 41, Application US/09419281
 ; Patent No. 6379926

GENERAL INFORMATION:
 APPLICANT: KREIDER, BRENT L.
 RUBEN, STEVEN M.
 OLSEN, HENRIK S.

TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC

COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/419,281
 FILING DATE: 15-Oct-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/995,156
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: STEEFE, ERIC K

REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0340004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 63 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 41:

US-09-419-281-41

Query Match 100.0%; Score 20; DB 4; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
 ||||
 Db 59 NLDA 62

APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280H1
CURRENT APPLICATION NUMBER: US/09/794,925
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-925-66

Query Match 100.0%; Score 20; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 1 NLDA 4

RESULT 6
US-09-681-442-66
Sequence 66, Application US/09681442
Patent No. US20020081634A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrichson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/681,442
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-681-442-66

Query Match 100.0%; Score 20; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 1 NLDA 4

RESULT 7
US-09-896-874-8
Sequence 8, Application US/09896874
Patent No. US20020016320A1
GENERAL INFORMATION:
APPLICANT: Fang, Lawrence Y.
APPLICANT: John, Varghese
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.40US01
CURRENT APPLICATION NUMBER: US/09/896,874
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-874-8

Query Match 100.0%; Score 20; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 4 NLDA 7

RESULT 8
US-09-896-139-8
Sequence 8, Application US/09896139
Patent No. US20020128255A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Frieskos, John N.
APPLICANT: Gallinas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mailhaid, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: Tenbrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.25US04
CURRENT APPLICATION NUMBER: US/09/896,139
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/252,736
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/255,956
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/268,497
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/279,779
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/295,589
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8

LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-139-8

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 4 NLDA 7

RESULT 9
US-09-895-843-8
Sequence 8, Application US/09895843
Patent No. US20020143177A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gallunas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mallalard, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: Tenbrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.41US01
CURRENT APPLICATION NUMBER: US/09/895, 843
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-895-843-8

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 4 NLDA 7

RESULT 10
US-09-795-903A-5
Sequence 5, Application US/09795903A
Patent No. US20020164760A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Lin, Xinh
APPLICANT: Koelsch, Gerald
TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
FILE REFERENCE: OMRP 179
CURRENT APPLICATION NUMBER: US/09/795,903A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/604,608
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-795-903A-5

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 4 NLDA 7

RESULT 11
US-09-794-927-63
Sequence 63, Application US/09794927
Patent No. US20010016324A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
FILE REFERENCE: 28341/6280DC
CURRENT APPLICATION NUMBER: US/09/794,927
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-63

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 4 NLDA 7

RESULT 12
US-09-795-847-63


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; Sequence 63, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-63
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```
Query Match          100.0%; Score 20; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 NLDA 4
    ||||
Db 4 NLDA 7
```

```
RESULT 13
US-09-794-743-63
; Sequence 63, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-63
```

```
Query Match          100.0%; Score 20; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NLDA 4
    ||||
Db 4 NLDA 7
```

```
RESULT 14
US-09-794-748-63
; Sequence 63, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-63
```

```
Query Match          100.0%; Score 20; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NLDA 4
    ||||
Db 4 NLDA 7
```

```
RESULT 15
US-09-796-264-5
; Sequence 5, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xunli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRP 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
```

;; PRIOR APPLICATION NUMBER: 09/604,608
;; PRIOR FILING DATE: 2000-06-27
;; PRIOR APPLICATION NUMBER: 60/168,060
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: 60/177,836
;; PRIOR FILING DATE: 2000-01-25
;; PRIOR APPLICATION NUMBER: 60/178,368
;; PRIOR FILING DATE: 2000-01-27
;; PRIOR APPLICATION NUMBER: 60/210,292
;; PRIOR FILING DATE: 2000-06-08
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-09-796-204-5

Query Match 100.0%; Score 20; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
DB 4 NLDA 7

RESULT 16
US-09-794-925-63
;; Sequence 63, Application US/09794925
;; Patent No. US20020064819A1
;; GENERAL INFORMATION:
;; APPLICANT: Gurney, Mark E.
;; APPLICANT: Bienkowski, Michael J.
;; APPLICANT: Heinrichson, Robert L.
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Yan, Riqiang
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USRS
;; FILE REFERENCE: 28341/6280H1
;; CURRENT APPLICATION NUMBER: US/09/794,925
;; PRIOR FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 63
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-63

Query Match 100.0%; Score 20; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
DB 4 NLDA 7

RESULT 17
US-09-681-442-63
;; Sequence 63, Application US/09681442
;; Patent No. US20020081634A1
;; GENERAL INFORMATION:
;; APPLICANT: Gurney, Mark E.
;; APPLICANT: Bienkowski, Michael J.
;; APPLICANT: Heinrichson, Robert L.
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Yan, Riqiang
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
;; FILE REFERENCE: 28341/6280FG
;; CURRENT APPLICATION NUMBER: US/09/681,442
;; PRIOR FILING DATE: 2001-04-05
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 63
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-63

Query Match 100.0%; Score 20; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
DB 4 NLDA 7

RESULT 18
US-09-845-226-5
;; Sequence 5, Application US/09845226
;; Patent No. US20020115600A1
;; GENERAL INFORMATION:
;; APPLICANT: Tang, Jordan J.N.
;; APPLICANT: Hong, Lin
;; APPLICANT: Ghosh, Arun K.
;; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
;; FILE REFERENCE: OMRF 182
;; CURRENT APPLICATION NUMBER: US/09/845,226
;; PRIOR FILING DATE: 2001-04-30
;; PRIOR APPLICATION NUMBER: 09/603,713
;; PRIOR FILING DATE: 2000-06-27
;; PRIOR APPLICATION NUMBER: 60/168,060
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: 60/177,836
;; PRIOR FILING DATE: 2000-01-25
;; PRIOR APPLICATION NUMBER: 60/178,368
;; PRIOR FILING DATE: 2000-01-27
;; PRIOR APPLICATION NUMBER: 60/210,292
;; PRIOR FILING DATE: 2000-06-08
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-845-226-5

Query Match 100.0%; Score 20; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 4 NLDA 7

RESULT 19
US-09-896-874-1
Sequence 1, Application US/09896874
Patent No. US2002016320A1
GENERAL INFORMATION:
APPLICANT: Fang, Lawrence Y.
APPLICANT: John, Varghese
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.40US01
CURRENT APPLICATION NUMBER: US/09/896,874
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-874-1

Query Match 100.0%; Score 20; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 4 NLDA 7

RESULT 20
US-09-896-139-1
Sequence 1, Application US/09896139
Patent No. US2002012825A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gallunas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mallalard, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: Tenbrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.25US04
CURRENT APPLICATION NUMBER: US/09/896,139
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/252,736
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/255,956
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/268,497
PRIOR FILING DATE: 2001-02-13

PRIOR APPLICATION NUMBER: US 60/279,779
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/295,589
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-139-1

Query Match 100.0%; Score 20; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 4 NLDA 7

RESULT 21
US-09-895-843-1
Sequence 1, Application US/09895843
Patent No. US2002014317A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gallunas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mallalard, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: Tenbrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.41US01
CURRENT APPLICATION NUMBER: US/09/895,843
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-895-843-1

Query Match 100.0%; Score 20; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 4 NLDA 7

RESULT 22
US-09-864-761-40453
Sequence 40453, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

```

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40453
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007981.43
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
; US-09-864-761-40453

Query Match          100.0%; Score 20; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
    ||||
Db 23 NIDA 26

RESULT 23
US-09-896-874-9
; Sequence 9, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.

```

```

; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40US01
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-896-874-9

Query Match          100.0%; Score 20; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
    ||||
Db 25 NIDA 28

RESULT 24
US-09-896-139-9
; Sequence 9, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John M.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mailaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: Tenbrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25US04
; CURRENT APPLICATION NUMBER: US/09/896,139
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-896-139-9

Query Match          100.0%; Score 20; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
    ||||

```

Db 25 NLDA 28

```
RESULT 25
US-09-895-843-9
; Sequence 9, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillalrd, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: Tenbrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-843-9
```

```
Query Match 100.0%; Score 20; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 NLDA 4
Db 25 NLDA 28

```
RESULT 26
US-09-896-874-4
; Sequence 4, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-4
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```
Query Match 100.0%; Score 20; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 NLDA 4
Db 25 NLDA 28

```
RESULT 27
US-09-896-139-4
; Sequence 4, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillalrd, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: Tenbrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25USU4
; CURRENT APPLICATION NUMBER: US/09/896,139
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-139-4
```

```
Query Match 100.0%; Score 20; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 NLDA 4
Db 25 NLDA 28

```
RESULT 28
US-09-895-843-4
; Sequence 4, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillalrd, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: Tenbrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
```

NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-895-843-4

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4
Db 25 NDA 28

RESULT 29
US-09-746-919-18
Sequence 18, Application US/09746919
Patent No. US20020013452A1
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
TITLE OF INVENTION: Pontzer, Carol H.
TITLE OF INVENTION: Interferon Tau Compositions and
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/746,919
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,467
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/438,753
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,891
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,741
FILING DATE: 09-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,050
FILING DATE: 02-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,890
FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 5600-0001.36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Amino acid sequence of fragment
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:4
US-09-746-919-18

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4
Db 6 NDA 9

RESULT 30
US-09-896-874-6
Sequence 6, Application US/09896874
Patent No. US20020016320A1
GENERAL INFORMATION:
APPLICANT: Fang, Lawrence Y.
TITLE OF INVENTION: John, Varghese
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.40US01
CURRENT APPLICATION NUMBER: US/09/896,874
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 33
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-874-6

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4
Db 28 NDA 31

RESULT 31
US-09-896-139-6
Sequence 6, Application US/09896139
Patent No. US20020128255A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
TITLE OF INVENTION: Hom, Roy
TITLE OF INVENTION: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Jagodzinska, Barbara
APPLICANT: Hom, Roy
APPLICANT: Galunas, Andrea
APPLICANT: Freskos, John M.
APPLICANT: Pullley, Shon R.
APPLICANT: Tenbrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.25US04
CURRENT APPLICATION NUMBER: US/09/896,139
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/252,736
PRIOR FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-896-139-6

Query Match 100.0%; Score 20; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
| | | |
Db 28 NLDA 31

RESULT 32
US-09-895-843-6
; Sequence 6, Application US/09895843
; Patent No. US2002014317A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallinas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mallalard, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: Tenbrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-895-843-6

Query Match 100.0%; Score 20; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
| | | |
Db 28 NLDA 31

RESULT 33
US-09-864-761-47026
; Sequence 47026, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47026
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005969.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.52
; US-09-864-761-47026

Query Match 100.0%; Score 20; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
| | | |
Db 7 NLDA 10

RESULT 34
US-09-864-761-38553
; Sequence 38553, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.

```
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38553
LENGTH: 39
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005237.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: SWISSPROT HIT: P22194, EVALU 2.00e-07
US-09-864-761-38553

Query Match      100.0%; Score 20; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42457
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011510.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
OTHER INFORMATION: EST_HUMAN HIT: BE148597.1, EVALU 2.00e-29
US-09-864-761-42457
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Query Match      100.0%; Score 20; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 36

US-09-864-761-41585

; Sequence 41585, Application US/09864761
; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263,6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,667

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 41585

; LENGTH: 63

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AL121771.17

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.5

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.7

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.5

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.1

; OTHER INFORMATION: EST-HUMAN HIT: A0130765.1, EVALUE 1.00e-30

; OTHER INFORMATION: SWISSPROT HIT: Q22712, EVALUE 1.50e+00

Best Local Similarity 100.0%; Pred. No. 77;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 NLDA 4
Db 24 NLDA 27

RESULT 37

US-10-107-371-1

; Sequence 1, Application US/10107371

; Patent No. US20020146390A1

; GENERAL INFORMATION:

; APPLICANT: White, John R.

; APPLICANT: Pelus, Louis M.

; TITLE OF INVENTION: Method of Treating Sepsis and ARDS Using Chemokine Beta-6 (as

; FILE REFERENCE: 1488.1520005

; CURRENT APPLICATION NUMBER: US/10/107,371

; CURRENT FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US 09/496,273

; PRIOR FILING DATE: 2000-02-01

; PRIOR APPLICATION NUMBER: US 08/852,212

; PRIOR FILING DATE: 1997-05-06

; PRIOR APPLICATION NUMBER: US 60/017,871

; PRIOR FILING DATE: 1996-05-14

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 70

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-107-371-1

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 70;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

Db 62 NLDA 65

RESULT 38

US-09-925-297-469

; Sequence 469, Application US/09925297

; Patent No. US20020081659A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA105

; CURRENT APPLICATION NUMBER: US/09/925,297

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05989

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 928

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 469

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (70)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-297-469

Query Match

Best Local Similarity 100.0%; Score 20; DB 10; Length 76;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

Db 52 NLDA 55

RESULT 39

US-09-764-877-1103
; Sequence 1103, Application US/09764877
; Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

PRIOR FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1103

LENGTH: 77

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (60)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (69)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-877-1103

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 77;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

Db 7 NLDA 10

RESULT 40

US-09-864-761-33423

; Sequence 33423, Application US/09864761

; Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aemica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 33423

LENGTH: 90

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC007041.3

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5

OTHER INFORMATION: EST_HUMAN HIT: A1114743.1, EVALUATE 1.00e-47

OTHER INFORMATION: SWISSPROT HIT: Q12446, EVALUATE 9.10e-01

US-09-864-761-33423

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

Db 50 NLDA 53

RESULT 41

US-09-970-921-2

; Sequence 2, Application US/0970921

; Patent No. US20020133845A1

GENERAL INFORMATION:

APPLICANT: Frank Michiels et al.

TITLE OF INVENTION: Improved Barstar Gene

FILE REFERENCE: 2428-0108P

CURRENT APPLICATION NUMBER: US/09/970,921

PRIOR FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 90

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: protein

US-09-970-921-2

Query Match
Best Local Similarity 100.0%; Score 20; DB 10; Length 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

Db 50 NLDA 53

Db 34 NLDA 37

RESULT 42

US-09-970-921-4
; Sequence 4, Application US/09970921
; Patent No. US2002013845A1
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: protein
US-09-970-921-4

Query Match 100.0%; Score 20; DB 10; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
|||||
Db 35 NLDA 38

RESULT 43

US-09-864-761-43579
; Sequence 43579, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43579
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens

; OTHER INFORMATION: MAP TO AC005541.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.89
; OTHER INFORMATION: EST_HUMAN HIT: AA354238.1, EVALUATE 9.00e-19
US-09-864-761-43579

Query Match 100.0%; Score 20; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
|||||
Db 31 NLDA 34

RESULT 44
US-09-775-938A-20
; Sequence 20, Application US/09775938A
; Patent No. US20020081665A1
; GENERAL INFORMATION:
; APPLICANT: Haygood, M.
; APPLICANT: Davidson, S.K.
; APPLICANT: Allen, S.W.
; APPLICANT: Hildebrand, M.
; TITLE OF INVENTION: Bystostatin, Bipyopyrans and Polyketides: Compositions and Meth
; FILE REFERENCE: 1133.010US1
; CURRENT APPLICATION NUMBER: US/09/775,938A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: PCT/US00/21326
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,283
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Endobugula sertula
US-09-775-938A-20

Query Match 100.0%; Score 20; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
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Db 69 NLDA 72

RESULT 45
US-09-974-298-4
; Sequence 4, Application US/09974298
; Patent No. US20020156263A1

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; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 755197CD1
US-09-974-298-4

Query Match          100.0%; Score 20; DB 9; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NDA 4
        ||||
Db      65 NDA 68
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Search completed: February 6, 2003, 11:39:48
Job time : 6.83333 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:59 : Search time 133.167 Seconds
(without alignments)
19.366 Million cell updates/sec

Title: PAT943-6
Perfect score: 20
Sequence: 1 nlda 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 7119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA.Main:*

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27: /cgn2_6/ptodata/1/paa/US60.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	4	1	PCT-US01-00797-66
2	20	100.0	4	1	PCT-US01-00798-66
3	20	100.0	4	18	US-09-416-901A-66
4	20	100.0	4	18	US-09-416-901B-66
5	20	100.0	4	19	US-09-548-365A-66
6	20	100.0	4	19	US-09-548-365D-66

7	20	100.0	4	19	US-09-548-366B-66	Sequence 66, Appl
8	20	100.0	4	19	US-09-548-366D-66	Sequence 66, Appl
9	20	100.0	4	19	US-09-548-368A-66	Sequence 66, Appl
10	20	100.0	4	19	US-09-548-368D-66	Sequence 66, Appl
11	20	100.0	4	19	US-09-548-369E-66	Sequence 66, Appl
12	20	100.0	4	19	US-09-548-370A-66	Sequence 66, Appl
13	20	100.0	4	19	US-09-548-370D-66	Sequence 66, Appl
14	20	100.0	4	19	US-09-548-370D-66	Sequence 66, Appl
15	20	100.0	4	19	US-09-548-372A-66	Sequence 66, Appl
16	20	100.0	4	19	US-09-548-372D-66	Sequence 66, Appl
17	20	100.0	4	19	US-09-548-376A-66	Sequence 66, Appl
18	20	100.0	4	19	US-09-548-376D-66	Sequence 66, Appl
19	20	100.0	4	19	US-09-551-853A-66	Sequence 66, Appl
20	20	100.0	4	19	US-09-551-853D-66	Sequence 66, Appl
21	20	100.0	4	20	US-09-668-314A-76	Sequence 76, Appl
22	20	100.0	4	20	US-09-668-314B-76	Sequence 76, Appl
23	20	100.0	4	20	US-09-681-442-66	Sequence 66, Appl
24	20	100.0	4	21	US-09-794-743-66	Sequence 66, Appl
25	20	100.0	4	21	US-09-794-748-66	Sequence 66, Appl
26	20	100.0	4	21	US-09-794-925-66	Sequence 66, Appl
27	20	100.0	4	21	US-09-794-927-66	Sequence 66, Appl
28	20	100.0	4	21	US-09-795-847-66	Sequence 66, Appl
29	20	100.0	4	22	US-09-869-414-66	Sequence 66, Appl
30	20	100.0	4	23	US-09-908-943A-142	Sequence 142, App
31	20	100.0	4	27	US-60-275-251-142	Sequence 142, App
32	20	100.0	5	1	PCT-US96-19549-2	Sequence 2, Appl1
33	20	100.0	5	8	US-08-485-152-2	Sequence 2, Appl1
34	20	100.0	5	18	US-09-471-669-51	Sequence 51, Appl
35	20	100.0	5	19	US-09-501-708-51	Sequence 51, Appl
36	20	100.0	5	21	US-09-723-739-51	Sequence 51, Appl
37	20	100.0	5	21	US-09-724-566-51	Sequence 51, Appl
38	20	100.0	5	21	US-09-724-566-51	Sequence 51, Appl
39	20	100.0	5	21	US-09-724-566-51	Sequence 51, Appl
40	20	100.0	5	21	US-09-724-566-51	Sequence 51, Appl
41	20	100.0	5	21	US-09-724-566-51	Sequence 51, Appl
42	20	100.0	8	16	PCT-US02-15590-257	Sequence 257, App
43	20	100.0	8	16	US-09-277-229-17	Sequence 17, Appl
44	20	100.0	8	20	US-09-668-314A-71	Sequence 71, Appl
45	20	100.0	9	18	US-09-471-669-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
PCT-US01-00797-66
Sequence 66, Application PC/TUS0100797
GENERAL INFORMATION:
APPLICANT: Blenkowski et al.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
FILE REFERENCE: 28341/6280M2
CURRENT APPLICATION NUMBER: PCT/US01/00797
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: 09/416,901
PRIORITY FILING DATE: 1999-10-13
PRIORITY APPLICATION NUMBER: 60/155,493
PRIORITY FILING DATE: 1999-09-23
PRIORITY APPLICATION NUMBER: 09/404,133
PRIORITY FILING DATE: 1999-09-23
PRIORITY APPLICATION NUMBER: PCT/US99/20881
PRIORITY FILING DATE: 1999-09-23
PRIORITY APPLICATION NUMBER: 60/101,594
PRIORITY FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
PCT-US01-00797-66

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NDA 4
||||
Db 1 NDA 4

RESULT 2
PCT-US01-00798-66
; Sequence 66, Application PC/TUS0100798

; GENERAL INFORMATION:
; APPLICANT: Bienkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280A1
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
PCT-US01-00798-66

Query Match 100.0%; Score 20; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NDA 4
||||
Db 1 NDA 4

RESULT 3
US-09-416-901A-66
; Sequence 66, Application US/09416901A
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280A
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-416-901A-66

Query Match 100.0%; Score 20; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NDA 4
||||
Db 1 NDA 4

RESULT 4
US-09-416-901B-66
; Sequence 66, Application US/09416901B
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280A
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-416-901B-66

Query Match 100.0%; Score 20; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NDA 4
||||
Db 1 NDA 4

RESULT 5
US-09-548-365A-66
; Sequence 66, Application US/09548365A
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
; FILE REFERENCE: 28341/6280E
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-548-365A-66
```

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Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NLDA 4
       ||||
Db       1 NLDA 4
```

```
RESULT 6
US-09-548-365D-66
; Sequence 66, Application US/09548365D
; GENERAL INFORMATION:
```

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; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280E
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-365D-66
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Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NLDA 4
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Db       1 NLDA 4
```

```
RESULT 7
US-09-548-366B-66
; Sequence 66, Application US/09548366B
; GENERAL INFORMATION:
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```
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280J
; CURRENT APPLICATION NUMBER: US/09/548,366B
; CURRENT FILING DATE: 2000-04-12
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; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-548-366B-66
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Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 NLDA 4
       ||||
Db       1 NLDA 4
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```
RESULT 8
US-09-548-366D-66
; Sequence 66, Application US/09548366D
; GENERAL INFORMATION:
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; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280J
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-366D-66
```

```
Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 NLDA 4
       ||||
Db       1 NLDA 4
```

```
RESULT 9
US-09-548-368A-66
; Sequence 66, Application US/09548368A
; GENERAL INFORMATION:
```

```
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
```

```
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 28341/6280C
;; CURRENT APPLICATION NUMBER: US/09/548,368A
;; CURRENT FILING DATE: 2000-04-12
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 71
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 66
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-548-368A-66
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 19; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NDA 4
    ||||
Db 1 NDA 4
```

```
RESULT 10
US-09-548-368D-66
; Sequence 66, Application US/09548368D
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280C
; CURRENT APPLICATION NUMBER: US/09/548,368D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-368D-66
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 19; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NDA 4
    ||||
Db 1 NDA 4
```

```
RESULT 11
US-09-548-369A-66
; Sequence 66, Application US/09548369A
; GENERAL INFORMATION:
```

```
;; APPLICANT: Gurney, Mark E.
;; APPLICANT: Bienkowski, Michael J.
;; APPLICANT: Heinrichson, Robert L.
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Yan, Riqiang
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 28341/6280G
;; CURRENT APPLICATION NUMBER: US/09/548,369A
;; CURRENT FILING DATE: 2000-04-12
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 71
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 66
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-548-369A-66
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 19; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NDA 4
    ||||
Db 1 NDA 4
```

```
RESULT 12
US-09-548-369E-66
; Sequence 66, Application US/09548369E
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
; FILE REFERENCE: 29915/6280G
; CURRENT APPLICATION NUMBER: US/09/548,369E
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-369E-66
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 19; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 NDA 4
    ||||
Db 1 NDA 4
```


RESULT 13

US-09-548-370A-66

; Sequence 66, Application US/09548370A

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrichson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR

; FILE REFERENCE: 28341/6280B

; CURRENT APPLICATION NUMBER: US/09/548,370A

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 66

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide

US-09-548-370A-66

Query Match

Best Local Similarity 100.0%; Score 20; DB 19; Length 4;

; FEATURE: Pred. No. 4.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4

Db 1 NDA 4

RESULT 14

US-09-548-370D-66

; Sequence 66, Application US/09548370D

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES THEREFOR

; FILE REFERENCE: 29915/6280B

; CURRENT APPLICATION NUMBER: US/09/548,370D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 66

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-09-548-370D-66

Query Match

Best Local Similarity 100.0%; Score 20; DB 19; Length 4;

; FEATURE: Pred. No. 4.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4

Db 1 NDA 4

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4

Db 1 NDA 4

RESULT 15

US-09-548-373A-66

; Sequence 66, Application US/09548373A

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrichson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR

; FILE REFERENCE: 28341/6280B

; CURRENT APPLICATION NUMBER: US/09/548,373A

; CURRENT FILING DATE: 2000-04-02

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 66

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide

US-09-548-373A-66

Query Match

Best Local Similarity 100.0%; Score 20; DB 19; Length 4;

; FEATURE: Pred. No. 4.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4

Db 1 NDA 4

RESULT 16

US-09-548-373D-66

; Sequence 66, Application US/09548373D

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES THEREFOR

; FILE REFERENCE: 29915/6280B

; CURRENT APPLICATION NUMBER: US/09/548,373D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 66

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-09-548-373D-66

Query Match

Best Local Similarity 100.0%; Score 20; DB 19; Length 4;

; FEATURE: Pred. No. 4.2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4

Db 1 NDA 4

```
; OTHER INFORMATION: Synthetic peptide
US-09-548-373D-66

Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4
   ||||
Db 1 NDA 4

RESULT 17
US-09-548-376A-66
; Sequence 66, Application US/09548376A
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USBS
; FILE REFERENCE: 28341/6280F
; CURRENT APPLICATION NUMBER: US/09/548,376A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-548-376A-66

Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4
   ||||
Db 1 NDA 4

RESULT 18
US-09-548-376D-66
; Sequence 66, Application US/09548376D
; GENERAL INFORMATION:
; APPLICANT: Gurney ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,376D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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; SOFTWARE: Patent In version 3.1
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
US-09-548-376D-66

Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4
   ||||
Db 1 NDA 4

RESULT 19
US-09-551-853A-66
; Sequence 66, Application US/09551853A
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
; FILE REFERENCE: 28341/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853A
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-551-853A-66

Query Match          100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NDA 4
   ||||
Db 1 NDA 4

RESULT 20
US-09-551-853D-66
; Sequence 66, Application US/09551853D
; GENERAL INFORMATION:
; APPLICANT: Gurney ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
```

PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-551-853D-66

Query Match 100.0%; Score 20; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 1 NLDA 4

RESULT 21
US-09-668-314A-76
Sequence 76, Application US/09668314A
GENERAL INFORMATION:
APPLICANT: Gurney, Mark
APPLICANT: Bienkowski, Michael J.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 28341/6280NCP
CURRENT APPLICATION NUMBER: US/09/668,314A
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/169,232
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 76
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-668-314A-76

Query Match 100.0%; Score 20; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 1 NLDA 4

RESULT 22
US-09-668-314B-76
Sequence 76, Application US/09668314B
GENERAL INFORMATION:
APPLICANT: Gurney, et al
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 28341/6280NCP

CURRENT APPLICATION NUMBER: US/09/668,314B
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/169,232
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-668-314B-76

Query Match 100.0%; Score 20; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 1 NLDA 4

RESULT 23
US-09-681-442-66
Sequence 66, Application US/09681442
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Helinikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 28341/6280FC
CURRENT APPLICATION NUMBER: US/09/681,442
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-681-442-66

Query Match 100.0%; Score 20; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||

Db 1 NLDA 4

RESULT 24
US-09-794-743-66
; Sequence 66, Application US/09794743
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-743-66

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 1 NLDA 4

RESULT 25
US-09-794-748-66
; Sequence 66, Application US/09794748
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-748-66

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 1 NLDA 4

RESULT 26
US-09-794-925-66
; Sequence 66, Application US/09794925
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-925-66

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 1 NLDA 4

RESULT 27
US-09-794-927-66
; Sequence 66, Application US/09794927
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR

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FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/794,927
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-927-66

Query Match          100.0%; Score 20; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
|||||
DB 1 NLDA 4

RESULT 28
US-09-795-847-66
; Sequence 66, Application US/09/95847
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-795-847-66

Query Match          100.0%; Score 20; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
|||||
```

```
DB 1 NLDA 4

RESULT 29
US-09-869-414-66
; Sequence 66, Application US/09869414
; GENERAL INFORMATION:
; APPLICANT: Bienkowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-869-414-66

Query Match          100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
|||||
DB 1 NLDA 4

RESULT 30
US-09-908-943A-142
; Sequence 142, Application US/09908943A
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-09-908-943A-142

Query Match          100.0%; Score 20; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 NIDA 4
||||
Db 1 NIDA 4

RESULT 31

US-60-275-251-142
; Sequence 142, Application US/60275251
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Helmricksen, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281
; CURRENT APPLICATION NUMBER: US/60/275,251
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-60-275-251-142

Query Match Best Local Similarity 100.0%; Score 20; DB 27; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
||||
Db 1 NIDA 4

RESULT 32

PCT-US96-19549-2
; Sequence 2, Application PC/TUS9619549
; GENERAL INFORMATION:
; APPLICANT: Athena Neurosciences, Inc.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/19549
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002230PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-19549-2

Query Match Best Local Similarity 100.0%; Score 20; DB 1; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
||||
Db 2 NIDA 5

RESULT 33

US-08-485-152-2
; Sequence 2, Application US/08485152
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Jacobson-Croak, Kirsten L.
; APPLICANT: Sinha, Sukanto
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,152
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-485-152-2

Query Match

Best Local Similarity 100.0%; Score 20; DB 8; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
||||
Db 2 NIDA 5

RESULT 34

US-09-471-669-51
; Sequence 51, Application US/09471669
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Guribai
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand

```

; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW
; CURRENT APPLICATION NUMBER: US/09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669-51

Query Match          100.0%; Score 20; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
    ||||
Db 2 NLDA 5

RESULT 35
US-09-501-708-51
; Sequence 51, Application US/09501708
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2
; CURRENT APPLICATION NUMBER: US/09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-708-51

Query Match          100.0%; Score 20; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
    ||||

```

```

Db 2 NLDA 5

RESULT 36
US-09-723-739-51
; Sequence 51, Application US/09723739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C3
; CURRENT APPLICATION NUMBER: US/09/723,739
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-739-51

Query Match          100.0%; Score 20; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
    ||||
Db 2 NLDA 5

RESULT 37
US-09-724-566-51
; Sequence 51, Application US/09724566
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C2
; CURRENT APPLICATION NUMBER: US/09/724,566
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104

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```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566-51

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
Db 2 NIDA 5

RESULT 38
US-09-724-568-51
; Sequence 51, Application US/09724568
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C5
; CURRENT APPLICATION NUMBER: US/09/724,568
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-568-51

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
Db 2 NIDA 5

RESULT 39
US-09-724-569-51
; Sequence 51, Application US/09724569
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
```

```

; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C6
; CURRENT APPLICATION NUMBER: US/09/724,569
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-571-51

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
Db 2 NIDA 5

RESULT 40
US-09-724-571-51
; Sequence 51, Application US/09724571
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW2C4
; CURRENT APPLICATION NUMBER: US/09/724,571
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-571-51

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
Db 2 NIDA 5

RESULT 41
```


PCT-US02-15590-257
; Sequence 257, Application PC/TUS0215590
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: BETA-SECRETASE SUBSTRATES AND USES
; FILE REFERENCE: 20886Y
; CURRENT APPLICATION NUMBER: PCT/US02/15590
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,591
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/316,115
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-Secretase Cleavage Site
PCT-US02-15590-257

Query Match 100.0%; Score 20; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
| | | |
Db 3 NIDA 6

RESULT 42
US-09-277-229-17
; Sequence 17, Application US/09277229
; GENERAL INFORMATION:
; APPLICANT: Ciltion, Martin
; APPLICANT: Vassar, Robert J.
; APPLICANT: Bennett, Brian D.
; TITLE OF INVENTION: Beta Secretase Genes and Polypeptides
; FILE REFERENCE: A-581
; CURRENT APPLICATION NUMBER: US/09/277,229
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-277-229-17

Query Match 100.0%; Score 20; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
| | | |
Db 3 NIDA 6

RESULT 43
US-09-668-314A-71
; Sequence 71, Application US/09668314A
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark
; APPLICANT: Bienkowski, Michael J.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314A

US-09-668-314A-71
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-668-314A-71

Query Match 100.0%; Score 20; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
| | | |
Db 3 NIDA 6

RESULT 44
US-09-668-314B-71
; Sequence 71, Application US/09668314B
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; FILE REFERENCE: 28341/6280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314B
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-668-314B-71

Query Match 100.0%; Score 20; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
| | | |
Db 3 NIDA 6

```

RESULT 45
US-09-471-669-52
; Sequence 52, Application US/09471669
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basil, Guribai
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NM
; CURRENT APPLICATION NUMBER: US/09/471,669
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-471-669-52

```

```

Query Match      100.0%; Score 20; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 NLDA 4
        |||
        4 NLDA 7

```

Search completed: February 6, 2003, 11:37:38
 Job time: 135.167 secs

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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:19:49 : Search time 14 Seconds
(without alignments)
23.165 Million cell updates/sec

Title: PAT943-6
Perfect score: 20
Sequence: 1 nlde 4

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues
Total number of hits satisfying chosen parameters: 845

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	20	100.0	4	US-09-668-314C-76	Sequence 76, Appl
2	20	100.0	4	US-09-794-925A-66	Sequence 66, Appl
3	20	100.0	4	US-09-794-927A-66	Sequence 66, Appl
4	20	100.0	4	US-09-869-414A-66	Sequence 66, Appl
5	20	100.0	4	US-09-548-366F-66	Sequence 66, Appl
6	20	100.0	5	US-09-724-566A-51	Sequence 51, Appl
7	20	100.0	5	US-09-471-669A-51	Sequence 51, Appl
8	20	100.0	8	US-09-668-314C-71	Sequence 71, Appl
9	20	100.0	9	PCT-US02-31846-8	Sequence 8, Appl
10	20	100.0	9	US-09-724-566A-52	Sequence 52, Appl
11	20	100.0	9	US-09-724-566A-83	Sequence 83, Appl
12	20	100.0	9	US-09-471-669A-52	Sequence 83, Appl
13	20	100.0	9	US-09-471-669A-83	Sequence 83, Appl
14	20	100.0	9	US-10-264-707-8	Sequence 8, Appl
15	20	100.0	9	US-10-160-777-8	Sequence 8, Appl
16	20	100.0	10	US-09-668-314C-63	Sequence 63, Appl
17	20	100.0	10	US-09-794-925A-63	Sequence 63, Appl
18	20	100.0	10	US-09-794-927A-63	Sequence 63, Appl
19	20	100.0	10	US-09-869-414A-63	Sequence 63, Appl
20	20	100.0	10	US-09-548-366F-63	Sequence 63, Appl
21	20	100.0	13	PCT-US02-31846-1	Sequence 1, Appl
22	20	100.0	13	US-10-264-707-1	Sequence 1, Appl
23	20	100.0	13	US-10-160-777-1	Sequence 1, Appl
24	20	100.0	30	PCT-US02-31846-9	Sequence 9, Appl
25	20	100.0	30	US-09-724-566A-53	Sequence 53, Appl
26	20	100.0	30	US-09-471-669A-53	Sequence 53, Appl

27	20	100.0	30	6	US-10-264-707-9	Sequence 9, Appl
28	20	100.0	30	6	US-10-160-777-9	Sequence 9, Appl
29	20	100.0	32	6	US-10-174-410-177	Sequence 177, App
30	20	100.0	32	6	US-10-174-410-180	Sequence 180, App
31	20	100.0	32	6	US-10-174-410-181	Sequence 181, App
32	20	100.0	32	6	US-10-174-410-198	Sequence 198, App
33	20	100.0	32	6	US-10-174-410-211	Sequence 211, App
34	20	100.0	32	6	US-10-174-410-214	Sequence 214, App
35	20	100.0	33	1	PCT-US02-31846-6	Sequence 6, Appl
36	20	100.0	33	5	US-09-724-566A-63	Sequence 63, Appl
37	20	100.0	33	5	US-09-471-669A-63	Sequence 63, Appl
38	20	100.0	33	6	US-10-264-707-6	Sequence 6, Appl
39	20	100.0	33	6	US-10-160-777-6	Sequence 6, Appl
40	20	100.0	34	1	PCT-US02-31846-4	Sequence 4, Appl
41	20	100.0	34	6	US-10-264-707-4	Sequence 4, Appl
42	20	100.0	34	6	US-10-160-777-4	Sequence 4, Appl
43	20	100.0	61	1	US-09-513-999C-5901	Sequence 5901, Ap
44	20	100.0	62	1	PCT-US02-32727-14180	Sequence 14180, A
45	20	100.0	62	6	US-10-057-498-14180	Sequence 14180, A

ALIGNMENTS

RESULT 1
US-09-668-314C-76
Sequence 76, Application US/09668314C
GENERAL INFORMATION:
APPLICANT: Gurney, et al
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
FILE REFERENCE: 28341/6280NC
CURRENT APPLICATION NUMBER: US/09/668,314C
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/169,232
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-668-314C-76
Query Match 100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 NLDA 4
OY 1 NLDA 4
DB 1 NLDA 4
RESULT 2
US-09-794-925A-66
Sequence 66, Application US/09794925A
GENERAL INFORMATION:
APPLICANT: Gurney et al
TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and US-
FILE REFERENCE: 29915/6280HI

```
; CURRENT APPLICATION NUMBER: US/09/794,925A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-794-925A-66
```

```
Query Match          100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NLDA 4
Db 1 NLDA 4
```

```
RESULT 3
US-09-794-927A-66
; Sequence 66, Application US/09794927A
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-794-927A-66
```

```
Query Match          100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NLDA 4
Db 1 NLDA 4
```

```
RESULT 4
US-09-869-414A-66
; Sequence 66, Application US/09869414A
```

```
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414A
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-869-414A-66
```

```
Query Match          100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NLDA 4
Db 1 NLDA 4
```

```
RESULT 5
US-09-548-366F-66
; Sequence 66, Application US/09548366F
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-366F-66
```

```
Query Match          100.0%; Score 20; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 NLDA 4
Db 1 NLDA 4
```

```
RESULT 6
US-09-724-566A-51
; Sequence 51, Application US/09724566A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Simha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-51

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 2 NLDA 5

RESULT 7
US-09-471-669A-51
; Sequence 51, Application US/09471669A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Simha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elian Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-00643005
; CURRENT FILING DATE: 1999-12-24
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 5
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669A-51

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 2 NLDA 5

RESULT 8
US-09-668-314C-71
; Sequence 71, Application US/09668314C
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; FILE REFERENCE: 28341/6280NCP
; CURRENT FILING DATE: 2000-09-22
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-668-314C-71

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 3 NLDA 6

RESULT 9
PCT-US02-31846-8
; Sequence 8, Application PC/TUS0231846
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-C
; CURRENT FILING DATE: 2002-11-19
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal biotin
; PCT-US02-31846-8

```

```

Query Match          100.0%; Score 20; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NLDA 4
    |||
Db 4 NLDA 7

```

RESULT 10

```

; Sequence 52, Application US/09724566A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guripal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
; US-09-724-566A-52

```

```

Query Match          100.0%; Score 20; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NLDA 4
    |||
Db 4 NLDA 7

```

RESULT 11

```

; Sequence 83, Application US/09724566A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guripal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese

```

```

; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: APP fragment P5-P4'wt
; US-09-724-566A-83

```

```

Query Match          100.0%; Score 20; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NLDA 4
    |||
Db 4 NLDA 7

```

RESULT 12

```

; Sequence 52, Application US/09471669A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guripal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-00643005
; CURRENT APPLICATION NUMBER: US/09/471,669A
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligopeptide substrate
; US-09-471-669A-52

```

Query Match 100.0% Score 20; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

OY 1 NLDA 4
1111
DB 4 NLDA 7

RESULT 13
US-09-471-669A-83

; Sequence 83, Application US/09471669A

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, Normand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; APPLICANT: Elan Pharmaceuticals, Inc.

; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS

; FILE REFERENCE: 015270-006430US

; CURRENT APPLICATION NUMBER: US/09/471,669A

; PRIOR FILING DATE: 1999-12-24

; PRIOR APPLICATION NUMBER: US 60/114,408

; PRIOR FILING DATE: 1998-12-31

; PRIOR APPLICATION NUMBER: US 60/119,571

; PRIOR FILING DATE: 1999-02-10

; PRIOR APPLICATION NUMBER: US 60/139,172

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 83

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: APP fragment P5-P4' wt

; US-09-471-669A-83

Query Match 100.0% Score 20; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
1111
DB 4 NLDA 7

RESULT 14
US-10-264-707-8

; Sequence 8, Application US/10264707

; GENERAL INFORMATION:

; APPLICANT: Fisher, Jed F.

; APPLICANT: Jacobs, Jon S.

; APPLICANT: Scherer, Brian S.

; TITLE OF INVENTION: Hydroxypropylamines

; FILE REFERENCE: 01-1555-B

; CURRENT APPLICATION NUMBER: US/10/264,707

; PRIOR FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: 60/327,149

; PRIOR FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: 60/334,058

; PRIOR FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

OY 1 NLDA 4
1111
DB 4 NLDA 7

RESULT 15
US-10-160-777-8

; Sequence 8, Application US/10160777

; GENERAL INFORMATION:

; APPLICANT: Freskos, John

; APPLICANT: Brown, David L.

; APPLICANT: Fobian, Yvette M.

; APPLICANT: Fang, Larry

; APPLICANT: Romero, Arthur G.

; APPLICANT: Varghese, John

; TITLE OF INVENTION: Hydroxy Alkyl Amines

; FILE REFERENCE: 01-1632-C

; CURRENT APPLICATION NUMBER: US/10/160,777

; PRIOR FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: 60/343,772

; PRIOR FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: 60/332,639

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/295,332

; PRIOR FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

; FEATURE:

; NAME/KEY: MISC_FEATURE

; LOCATION: (1)-(1)

; OTHER INFORMATION: N-terminal biotin

; US-10-160-777-8

Query Match 100.0% Score 20; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
1111
DB 4 NLDA 7

RESULT 16
US-09-668-314C-63

; Sequence 63, Application US/09668314C

; GENERAL INFORMATION:

; APPLICANT: Guiney, et al

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US

; FILE REFERENCE: 28341/6280NCP

; CURRENT APPLICATION NUMBER: US/09/668,314C

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US 60/169,232

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

; FEATURE:

; NAME/KEY: MISC_FEATURE

; LOCATION: (1)-(1)

; OTHER INFORMATION: N-terminal biotin

; US-10-160-777-8

```

; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-668-114C-63
```

```
Query Match          100.0%; Score 20; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NLDA 4
        ||||
Db       4 NLDA 7
```

```

RESULT 17
US-09-794-925A-63
; Sequence 63, Application US/09794925A
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-794-925A-63
```

```
Query Match          100.0%; Score 20; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NLDA 4
        ||||
Db       4 NLDA 7
```

```

RESULT 18
US-09-794-927A-63
; Sequence 63, Application US/09794927A
; GENERAL INFORMATION:
```

```

; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Use
; FILE REFERENCE: 29915/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-794-927A-63
```

```
Query Match          100.0%; Score 20; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NLDA 4
        ||||
Db       4 NLDA 7
```

```

RESULT 19
US-09-869-414A-63
; Sequence 63, Application US/09869414A
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414A
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-869-414A-63
```

```
Query Match          100.0%; Score 20; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 NLDA 4
        ||||
Db       4 NLDA 7
```


RESULT 20
US-09-548-366F-63
; Sequence 63, Application US/09548366F
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62807
; CURRENT APPLICATION NUMBER: US/09/548,366F
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-366F-63

Query Match 100.0%; Score 20; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 4 NLDA 7

RESULT 21
PCT-US02-31846-1
; Sequence 1, Application PC/TUS0231846
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-C
; CURRENT APPLICATION NUMBER: PCT/US02/31846
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; NAME/KEY: MISC_FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: covalent attachment of oregon green
PCT-US02-31846-1

Query Match 100.0%; Score 20; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 4 NLDA 7

RESULT 22
US-10-264-707-1
; Sequence 1, Application US/10264707
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-B
; CURRENT APPLICATION NUMBER: US/10/264,707
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; NAME/KEY: MISC_FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: covalent attachment of oregon green
US-10-264-707-1

Query Match 100.0%; Score 20; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 4 NLDA 7

RESULT 23
US-10-160-777-1
; Sequence 1, Application US/10160777
; GENERAL INFORMATION:
; APPLICANT: Freskos, John
; APPLICANT: Brown, David L.
; APPLICANT: Fobian, Yvette M.
; APPLICANT: Fang, Larry
; APPLICANT: Romero, Arthur G.
; APPLICANT: Varghese, John
; TITLE OF INVENTION: Hydroxy Alkyl Amines
; FILE REFERENCE: 01-1632-C
; CURRENT APPLICATION NUMBER: US/10/160,777
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/343,772
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 60/332,639
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/295,332
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13

```

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: covalent attachment of oregon green
US-10-160-777-1

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 4 NLDA 7

RESULT 24
PCT-US02-31846-9
; Sequence 9, Application PC/TUS0231846
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-C
; CURRENT APPLICATION NUMBER: PCT/US02/31846
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
PCT-US02-31846-9

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 25 NLDA 28

RESULT 25
US-09-724-566A-53
; Sequence 53, Application US/09724566A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
```

```

; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide substrate
US-09-724-566A-53

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 25 NLDA 28

RESULT 26
US-09-471-669A-53
; Sequence 53, Application US/09471669A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Guribbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-0064300S
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-471-669A-53

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 25 NLDA 28
```

RESULT 27
US-10-264-707-9
; Sequence 9, Application US/10264707
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-155-B
; CURRENT APPLICATION NUMBER: US/10/264,707
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-264-707-9

Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
||||
Db 25 NIDA 28

RESULT 28
US-10-160-777-9
; Sequence 9, Application US/10160777
; GENERAL INFORMATION:
; APPLICANT: Freskos, John
; APPLICANT: Brown, David L.
; APPLICANT: Fobian, Yvette M.
; APPLICANT: Fang, Larry
; APPLICANT: Romero, Arthur G.
; APPLICANT: Varigheze, John
; TITLE OF INVENTION: Hydroxy Alkyl Amines
; FILE REFERENCE: 01-1632-C
; CURRENT APPLICATION NUMBER: US/10/160,777
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/343,772
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 60/332,639
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/295,332
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-160-777-9

Query Match 100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
||||
Db 25 NIDA 28

RESULT 29
US-10-174-410-177
; Sequence 177, Application US/10174410
; GENERAL INFORMATION:
; APPLICANT: Louie, Gordon V.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
; FILE REFERENCE: 524982000300
; CURRENT APPLICATION NUMBER: US/10/174,410
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/299,058
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 336
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Catharanthus roseus
US-10-174-410-177

Query Match 100.0%; Score 20; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
||||
Db 23 NIDA 26

RESULT 30
US-10-174-410-180
; Sequence 180, Application US/10174410
; GENERAL INFORMATION:
; APPLICANT: Louie, Gordon V.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
; FILE REFERENCE: 524982000300
; CURRENT APPLICATION NUMBER: US/10/174,410
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/299,058
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 336
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-174-410-180

Query Match 100.0%; Score 20; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
||||
Db 23 NIDA 26

RESULT 31
US-10-174-410-191
; Sequence 191, Application US/10174410
; GENERAL INFORMATION:
; APPLICANT: Louie, Gordon V.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Gajiwala, Ketan S.
US-10-174-410-191

```
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
FILE REFERENCE: 524982000300
CURRENT APPLICATION NUMBER: US/10/174,410
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/299,058
NUMBER OF SEQ ID NOS: 336
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 191
LENGTH: 32
TYPE: PRT
ORGANISM: L. innocua
US-10-174-410-191
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NIDA 4
    |||
Db 23 NIDA 26
```

```
RESULT 32
US-10-174-410-198
Sequence 198, Application US/10174410
GENERAL INFORMATION:
APPLICANT: Louie, Gordon V.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
FILE REFERENCE: 524982000300
CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/299,058
NUMBER OF SEQ ID NOS: 336
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 32
TYPE: PRT
ORGANISM: L. monocytogenes
US-10-174-410-198
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NIDA 4
    |||
Db 23 NIDA 26
```

```
RESULT 33
US-10-174-410-211
Sequence 211, Application US/10174410
GENERAL INFORMATION:
APPLICANT: Louie, Gordon V.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
FILE REFERENCE: 524982000300
CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/299,058
NUMBER OF SEQ ID NOS: 336
```

```
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 32
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-174-410-211
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NIDA 4
    |||
Db 23 NIDA 26
```

```
RESULT 34
US-10-174-410-214
Sequence 214, Application US/10174410
GENERAL INFORMATION:
APPLICANT: Louie, Gordon V.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Sauder, J. Michael
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF
FILE REFERENCE: 524982000300
CURRENT APPLICATION NUMBER: US/10/174,410
CURRENT FILING DATE: 2002-06-17
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/299,058
NUMBER OF SEQ ID NOS: 336
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 214
LENGTH: 32
TYPE: PRT
ORGANISM: Treponema pallidum
US-10-174-410-214
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NIDA 4
    |||
Db 23 NIDA 26
```

```
RESULT 35
PCT-US02-31846-6
Sequence 6, Application PC/TUS0231846
GENERAL INFORMATION:
APPLICANT: Fisher, Jed F.
APPLICANT: Jacobs, Jon S.
APPLICANT: Scherer, Brian S.
TITLE OF INVENTION: Hydroxypropylamines
FILE REFERENCE: 01-1555-C
CURRENT APPLICATION NUMBER: PCT/US02/31846
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/327,149
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/334,058
PRIOR FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 33
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
FEATURE:
NAME/KEY: MISC_FEATURE
```

```
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
PCT-US02-31846-6

Query Match          100.0%; Score 20; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLDA 4
       1111
Db      28 NLDA 31

RESULT 36
US-09-724-566A-63
; Sequence 63, Application US/09724566A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEMC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P26-P4'sw peptide substrate
US-09-724-566A-63

Query Match          100.0%; Score 20; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLDA 4
       1111
Db      28 NLDA 31

RESULT 37
US-09-471-669A-63
; Sequence 63, Application US/09471669A
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
```

```
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; CURRENT FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 63
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P26-P4'sw peptide substrate
US-09-471-669A-63

Query Match          100.0%; Score 20; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLDA 4
       1111
Db      28 NLDA 31

RESULT 38
US-10-264-707-6
; Sequence 6, Application US/10264707
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-B
; CURRENT APPLICATION NUMBER: US/10/264,707
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
US-10-264-707-6

Query Match          100.0%; Score 20; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NLDA 4
       1111
Db      28 NLDA 31

RESULT 39
US-10-160-777-6
; Sequence 6, Application US/10160777
; GENERAL INFORMATION:
; APPLICANT: Freskos, John
```

```

; APPLICANT: Brown, David L.
; APPLICANT: Fobian, Yvette M.
; APPLICANT: Fang, Larry
; APPLICANT: Romero, Arthur G.
; APPLICANT: Varghese, John
; TITLE OF INVENTION: Hydroxy Alkyl Amines
; FILE REFERENCE: 01-1632-C
; CURRENT APPLICATION NUMBER: US/10/160,777
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/343,772
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 60/332,639
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/295,332
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; US-10-160-777-6
```

```
Query Match          100.0%; Score 20; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NDA 4
    ||||
Db 28 NDA 31
```

```

RESULT 40
PCT-US02-31846-4
; Sequence 4, Application PC/TUS0231846
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-C
; CURRENT APPLICATION NUMBER: PCT/US02/31846
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (32)..(32)
; OTHER INFORMATION: covalent attachment of oregon green
; PCT-US02-31846-4
```

```
Query Match          100.0%; Score 20; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e+02;
```

```
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NDA 4
    ||||
Db 25 NDA 28
```

```

RESULT 41
US-10-264-707-4
; Sequence 4, Application US/10264707
; GENERAL INFORMATION:
; APPLICANT: Fisher, Jed F.
; APPLICANT: Jacobs, Jon S.
; APPLICANT: Scherer, Brian S.
; TITLE OF INVENTION: Hydroxypropylamines
; FILE REFERENCE: 01-1555-B
; CURRENT APPLICATION NUMBER: US/10/264,707
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/327,149
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/334,058
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (32)..(32)
; OTHER INFORMATION: covalent attachment of oregon green
; US-10-264-707-4
```

```
Query Match          100.0%; Score 20; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 NDA 4
    ||||
Db 25 NDA 28
```

```

RESULT 42
US-10-160-777-4
; Sequence 4, Application US/10160777
; GENERAL INFORMATION:
; APPLICANT: Freskos, John
; APPLICANT: Brown, David L.
; APPLICANT: Fobian, Yvette M.
; APPLICANT: Fang, Larry
; APPLICANT: Romero, Arthur G.
; APPLICANT: Varghese, John
; TITLE OF INVENTION: Hydroxy Alkyl Amines
; FILE REFERENCE: 01-1632-C
; CURRENT APPLICATION NUMBER: US/10/160,777
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/343,772
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 60/332,639
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/295,332
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 34
```

```

: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: synthetic peptide
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (1)..(1)
: OTHER INFORMATION: N-terminal biotin
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (32)..(32)
: OTHER INFORMATION: covalent attachment of oregon green
US-10-160-777-4

```

```

Query Match          100.0%; Score 20; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NLDA 4
Db 25 NLDA 28

```

```

RESULT 43
US-09-513-999C-5901
: Sequence 5901, Application US/09513999C
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Duclert, A.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: Expresed Sequence Tags and Encoded Human Proteins.
: FILE REFERENCE: 59, US2, REG
: CURRENT APPLICATION NUMBER: US/09/513, 999C
: CURRENT FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/122,487
: NUMBER OF SEQ ID NOS: 1999-02-26
: SOFTWARE: Patent.ppm
: SEQ ID NO 5901
: LENGTH: 61
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: UNSURE
: LOCATION: 24
: OTHER INFORMATION: Xaa-His or Gln
: FEATURE:
: NAME/KEY: UNSURE
: LOCATION: 59
: OTHER INFORMATION: Xaa-Ala or Gly or Pro or Arg
US-09-513-999C-5901

```

```

Query Match          100.0%; Score 20; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NLDA 4
Db 31 NLDA 34

```

```

RESULT 44
PCT-US02-32727-14180
: Sequence 14180, Application PC/TUS0232727
: GENERAL INFORMATION:
: APPLICANT: Mitcham, Jennifer
: APPLICANT: Skeiky, Yasir
: APPLICANT: Persing, David
: APPLICANT: Bhatia, Ajay
: APPLICANT: Maisonneuve, Jean Francois
: APPLICANT: Zhang, Yanni
: APPLICANT: Wang, Siqing
: APPLICANT: Jen, Shylan

```

```

: APPLICANT: Lodes, Michael
: APPLICANT: Benson, Darin
: APPLICANT: Jones, Robert
: APPLICANT: Carter, Darick
: APPLICANT: Barth, Brenda
: APPLICANT: Douglas, John
: TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acn
: FILE REFERENCE: 210121.514C1
: CURRENT APPLICATION NUMBER: PCT/US02/32727
: CURRENT FILING DATE: 2002-10-11
: NUMBER OF SEQ ID NOS: 30992
: SEQ ID NO 14180
: LENGTH: 62
: TYPE: PRT
: ORGANISM: Propionl acnes
PCT-US02-32727-14180

```

```

Query Match          100.0%; Score 20; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NLDA 4
Db 8 NLDA 11

```

```

RESULT 45
US-10-057-498-14180
: Sequence 14180, Application US/10057498
: GENERAL INFORMATION:
: APPLICANT: Mitcham, Jennifer
: APPLICANT: Skeiky, Yasir
: APPLICANT: Persing, David
: TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acn
: FILE REFERENCE: 210121.514
: CURRENT APPLICATION NUMBER: US/10/057,498
: CURRENT FILING DATE: 2001-04-20
: NUMBER OF SEQ ID NOS: 29212
: SEQ ID NO 14180
: LENGTH: 62
: TYPE: PRT
: ORGANISM: Propionl acnes
US-10-057-498-14180

```

```

Query Match          100.0%; Score 20; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NLDA 4
Db 8 NLDA 11

```

```

Search completed: February 6, 2003, 11:39:04
Job time : 14 secs

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 : Search time 10.5 Seconds
(without alignments)
36.623 Million cell updates/sec

Title: PAT943-6
Perfect score: 20
Sequence: 1 nlda 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1503

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_73:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	53	2	S43965
2	20	100.0	54	2	C72809
3	20	100.0	68	2	A88030
4	20	100.0	70	2	S58932
5	20	100.0	72	2	C89933
6	20	100.0	73	2	H90802
7	20	100.0	75	1	BVECRX
8	20	100.0	75	2	H81320
9	20	100.0	82	2	JC4205
10	20	100.0	82	2	T09234
11	20	100.0	85	1	GDEC
12	20	100.0	85	2	A99745
13	20	100.0	85	2	E85585
14	20	100.0	88	2	A38085
15	20	100.0	89	2	E97731
16	20	100.0	90	1	S01373
17	20	100.0	91	1	C69973
18	20	100.0	91	2	A55406
19	20	100.0	91	2	A97004
20	20	100.0	93	2	AB0449
21	20	100.0	95	2	A81176
22	20	100.0	96	2	A57483
23	20	100.0	102	2	C84003
24	20	100.0	103	2	A85821
25	20	100.0	103	2	E90973
26	20	100.0	103	2	E72664
27	20	100.0	109	2	S50356
28	20	100.0	110	2	S65003
29	20	100.0	112	2	A75544

30	20	100.0	114	2	AC0725	conserved hypothe
31	20	100.0	114	2	AF0252	conserved hypothe
32	20	100.0	114	2	H89785	hypothetical prote
33	20	100.0	115	2	D32227	hypothetical prote
34	20	100.0	116	2	T44504	merp protein (lipo
35	20	100.0	116	2	T45512	probable transport
36	20	100.0	116	2	C64562	hypothetical prote
37	20	100.0	119	2	F83714	holo-(acyl carrier
38	20	100.0	123	2	S55326	pseudazurin - Thi
39	20	100.0	125	2	C38286	hypothetical prote
40	20	100.0	126	2	S53340	CD59 protein - rat
41	20	100.0	126	2	T18655	hypothetical prote
42	20	100.0	126	2	AH1425	hypothetical secre
43	20	100.0	127	2	AG1425	hypothetical secre
44	20	100.0	129	2	AE1933	hypothetical prote
45	20	100.0	129	2	AC0782	probable DNA-bind

ALIGNMENTS

RESULT 1
S43965
hypothetical protein (clone PRK21) - Rhizobium sp. (strain NGR234) (fragment)
C:Species: Rhizobium sp.
A:Variety: strain NGR234
C>Date: 20-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 02-Jul-1998
C:Accession: S43965
R:Perrel, X.; Fellay, R.; Bjourson, A.J.; Cooper, J.E.; Brenner, S.; Broughton, W.J.
Nucleic Acids Res. 22, 1335-1341, 1994
A:Title: Subtraction hybridisation and shot-gun sequencing: a new approach to identifi
A:Reference number: S43961; MUID:9448027; PMID:8190622
A:Accession: S43965
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-53 <PER>
A:Experimental source: strain NGR234
C:Superfamily: inner membrane protein malK; ATP-binding cassette homology
C:Keywords: ATP
F:1-53/Domain: ATP-binding cassette homology (fragment) <ABC>

Query Match 100.0%; Score 20; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 35 NLDA 38

RESULT 2
C72809
gp87 protein - Mycobacterium phage D29
C:Species: Mycobacterium phage D29
C>Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 20-Apr-2001
C:Accession: C72809
R:Ford, W.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 279, 143-164, 1998
A:Title: Genome structure of mycobacteriophage D29: Implications for phage evolution
A:Reference number: A72800; MUID:98300335; PMID:9636706
A:Accession: C72809
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-54 <FOR>
A:Cross-references: GB:AF022214; NID:g3172250; PIDN:AAC18517.1; PID:g3172324
C:Genetics:
A:Gene: 87

Query Match 100.0%; Score 20; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

Db 9 NUDA 12

RESULT 3

A:Accession: C89933
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
R:Anonymous, The C. elegans Sequencing Consortium.
A:Title: Genome Sequence of the nematode *C. elegans*: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Accession: A88030
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <STO>
A:Cross-references: GB:chr_II; PIDN:AC78187.1; PID:93866036; GSPDB:GN00020; CESP:F46F5.6
C:Genetics:
A:Gene: F46F5.8
A:Map position: 2

Query Match 100.0%; Score 20; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NUDA 4
1111
Db 32 NUDA 35

RESULT 4

S58932
DNA-directed RNA polymerase (EC 2.7.7.6) Chain ABC10 alpha - yeast (*Saccharomyces cerevisiae*)
A:Alternate names: protein YHR143W-a; RPC10 protein
C:Species: *Saccharomyces cerevisiae*
C:Date: 28-Nov-1995 #sequence_revision 09-Mar-1996 #text_change 02-Jun-2000
C:Accession: S58932; S58934; S58515
R:Reich, I.; Carles, C.; Riva, M.; Sentenac, A.
Gene Expr. 2, 31-37, 1992
A:Title: RPC10 encodes a new mini subunit shared by yeast nuclear RNA polymerases.
A:Reference number: S58932; MUID:92314714; PMID:1617300
A:Accession: S58932
A:Molecule type: DNA
A:Residues: 1-70 <TR>
A:Cross-references: EMBL:U23378; NID:g733517; PIDN:AA64417.1; PID:g733518
A:Accession: S58934
A:Molecule type: protein
A:Residues: 4-22;64-69 <TRW>
C:Genetics:
A:Gene: SGD:RPB12; RPC10
A:Cross-references: MIPS:YHR143W-a; SGD:S0001185
A:Map position: 8R
A:Note: YHR143W-a
C:Superfamily: DNA-directed RNA polymerase chain ABC10 alpha
C:Keywords: nucleotidyltransferase; nucleus; transcription

Query Match 100.0%; Score 20; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NUDA 4
1111
Db 11 NUDA 14

RESULT 5

C89933
hypothetical protein [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89933
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C

ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuka, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-72 <KUR>
A:Cross-references: GB:BA000018; PID:g13701330; PIDN:BA042624.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1362

Query Match 100.0%; Score 20; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NUDA 4
1111
Db 20 NUDA 23

RESULT 6

H90802
hypothetical protein Ecs1392 [imported] - *Escherichia coli* (strain O157:H7, substrain
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: H90802
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurikawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuharu, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and 9
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90802
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-73 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034815.1; PID:g13360852; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: Ecs1392

Query Match 100.0%; Score 20; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NUDA 4
1111
Db 67 NUDA 70

RESULT 7

BVECRY
tray protein - *Escherichia coli* plasmids
C:Species: *Escherichia coli*
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C:Accession: C25033; C32014
R:Finlay, B.B.; Frost, L.S.; Paranchych, W.
J. Bacteriol. 168, 132-139, 1986
A:Title: Origin of transfer of IncF plasmids and nucleotide sequences of the type II
A:Reference number: A25033; MUID:87008371; PMID:3531163
A:Accession: C25033
A:Molecule type: DNA
A:Residues: 1-75 <FIN>
A:Cross-references: GB:M15136; NID:g151788; PIDN:AA26076.1; PID:g151789
A:Experimental source: plasmid R100-1
R:Imamoto, S.; Yoshioke, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A:Title: Identification and characterization of the products from the *tray* and *tray g*

A:Reference number: A32014; MUID:88227859; PMID:2836369

A:Accession: C32014

A:Molecule type: DNA

A:Residues: 1-75 <INA>

A:Cross-references: GB:M20941; NID:g151778; PIDN:AAA26073.1; PID:g151781

A:Experimental source: plasmid R100

A:Genetics: tray

A:Genome: plasmid

A:Start codon: TTG

C:Function:

A:Description: involved in the conjugation process of bacterial cells for the exchange of

C:Superfamily: tray protein

C:Keywords: DNA binding; pilin formation; plasmid transfer

Query Match 100.0%; Score 20; DB 1; Length 75;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4

Db 57 NLDA 60

RESULT 8

H81320 small hydrophobic protein Cj1158c [Imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C:Accession: H81320

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanvliet, A.; Whitehead, S.; Barrall

Nature 403, 665-668, 2000

A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: H81320

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-75 <PAR>

A:Cross-references: GB:AL139077; GB:AL111168; NID:96968444; PIDN:CA873412.1; PID:9696859

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj1158c

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 75;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4

Db 6 NLDA 9

RESULT 9

JC4205 hypothetical 9.1k protein - Frankia sp.

C:Species: Frankia sp.

C>Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 22-Oct-1999

C:Accession: JC4205

R:Harriott, O.T.; Hosted, T.J.; Benson, D.R.

Gene 161, 63-67, 1995

A>Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fixatio

A:Reference number: JC4203; MUID:95369734; PMID:7642138

A:Accession: JC4205

A:Molecule type: DNA

A:Residues: 1-82 <HAR>

A:Cross-references: GB:L29299; NID:g497430; PIDN:AA082972.1; PID:g497433

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 82;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4

Db 17 NLDA 20

RESULT 10

T09234

hypothetical protein 1 - Frankia alni

C:Species: Frankia alni

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T09234

R:Benson, D.R.

submitted to the EMBL Data Library, November 1998

A:Reference number: 216624

A:Accession: T09234

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-82 <BEN>

A:Cross-references: EMBL:L29299; NID:g3953454; PID:g497433

A:Experimental source: strain cpil

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 82;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4

Db 17 NLDA 20

RESULT 11

glutaredoxin 1 - Escherichia coli (strain K-12)

N:Alternate names: thioltransferase

C:Species: Escherichia coli

C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 01-Mar-2002

C:Accession: A00283; A24397; I59418; A64823; A39568

R:Hoeeog, J.O.; Joernvall, H.; Holmgren, A.; Carlquist, M.; Petsson, M.

Eur. J. Biochem. 136, 223-232, 1983

A>Title: The primary structure of Escherichia coli glutaredoxin. Distant homology wit

A:Reference number: A00283; MUID:84004402; PMID:6352262

A:Accession: A00283

A:Molecule type: protein

A:Residues: 1-85 <HO1>

A:Experimental source: K-12, strain C10-17

R:Hoeeog, J.O.; von Bahr-Lindstroem, H.; Joernvall, H.; Holmgren, A.

Gene 43, 13-21, 1986

A>Title: Cloning and expression of the glutaredoxin (grx) gene of Escherichia coli.

A:Reference number: A24397; MUID:87005940; PMID:3530878

A:Accession: A24397

A:Molecule type: DNA

A:Residues: 1-85 <HO2>

A:Cross-references: GB:M13449; NID:g146272; PIDN:AAA23936.1; PID:g146273

R:Chatterjee, P.K.; Sternberg, N.L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8950-8954, 1995

A>Title: A general genetic approach in Escherichia coli for determining the mechanism

A:Reference number: I59418; MUID:96004656; PMID:7568050

A:Accession: I59418

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-85 <RES>

A:Cross-references: EMBL:U18655; NID:g609323; PIDN:AA03449.1; PID:g609325

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.: Rose, D.J.; Mau, B.; Siao, Y.

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A64823

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-85 <BLAT>

A:Cross-references: GB:AE000187; GB:U00096; NID:g1787070; PIDN:AA03449.1; PID:g1787070

A:Experimental source: strain K-12, substrain MG1655

R:Sandberg, V.A.; Kren, B.; Fuchs, J.A.; Woodward, C.

Biochemistry 30, 5475-5484, 1991
A:Title: Escherichia coli glutaredoxin: cloning and overexpression, thermodynamic stability
A:Reference number: A39568; PMID:91242463; PMID:2036416
A:Accession: A39568
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 'MRREI', 1-15 <SANS>
C:Genetics:
A:Gene: grxA; grx
A:Map position: 19 mln
C:Function:
A:Description: the disulfide bond functions as an electron carrier in the glutathione-dependent, it is also involved in reducing some disulfides in a coupled system with glutathion
A:Pathway: deoxyribonucleotide biosynthesis
C:Superfamily: glutaredoxin; glutaredoxin homology
C:Keywords: deoxyribonucleotide biosynthesis; electron transfer; monomer; redox-active d
F:11-14/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 20; DB 1; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
|||
Db 82 NIDA 85

RESULT 12
A99745
hypothetical protein Ecs0929 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 30-Jun-2002
C:Accession: A99745
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gesawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; PMID:21156231; PMID:11258796
A:Accession: A99745
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-85 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA834352.1; PID:G13360388; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: Ecs0929
C:Superfamily: glutaredoxin; glutaredoxin homology
C:Keywords: redox-active disulfide
F:11-14/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
|||
Db 82 NIDA 85

RESULT 13
E85595
hypothetical protein grxA [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 30-Jun-2002
C:Accession: E85595
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Hiller, D.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; PMID:21074935; PMID:11206551
A:Accession: E85595
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-85 <STO>
A:Cross-references: GB:AE005174; NID:G1513864; PIDN:AAG55225.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: grxA
C:Superfamily: glutaredoxin; glutaredoxin homology
C:Keywords: redox-active disulfide
F:11-14/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 20; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
|||
Db 82 NIDA 85

RESULT 14
A38085
S-layer glycoprotein - Haloferax volcanii (fragments)
C:Species: Haloferax volcanii
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 04-Sep-1998
C:Accession: A38085
R:Mengele, R.; Sumper, M.
J. Biol. Chem. 267, 8182-8185, 1992
A:Title: Drastic differences in glycosylation of related S-layer glycoproteins from m
A:Reference number: A38085; PMID:9235030; PMID:1569073
A:Accession: A38085
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-88 <MEN>
C:Superfamily: S-layer glycoprotein
C:Keywords: glycoprotein

Query Match 100.0%; Score 20; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
|||
Db 2 NIDA 5

RESULT 15
E97731
hypothetical protein RC0253 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: E97731
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; PMID:2142074; PMID:11557893
A:Accession: E97731
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <KUR>
A:Cross-references: GB:AE006914; PIDN:AAL02791.1; PID:G15619308; GSPDB:GN00173
C:Genetics:
A:Gene: RC0253

Query Match 100.0%; Score 20; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
|||
Db 35 NIDA 38

RESULT 16

S01373
 ribonuclease inhibitor - Bacillus amyloliquefaciens
 N:Alternate names: barstar
 C:Species: Bacillus amyloliquefaciens
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S01373
 J: Hartley, R.W.
 J: Mol. Biol. 202, 913-915, 1988
 A:Title: Barnase and barstar. Expression of its cloned inhibitor permits expression of a
 A:Reference number: S01372; MUID:99012012; PMID:3050134
 A:Accession: S01373
 A:Molecule type: DNA
 A:Residues: 1-90 <HAR>
 A:Cross-references: EMBL:X15545; NID:g1155006; PIDN:CA33551.1; PID:g39312
 C:Superfamily: Bacillus ribonuclease inhibitor

Query Match 100.0%; Score 20; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 34 NLDA 37

RESULT 17
 ribonuclease inhibitor homolog yrdF - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: C69973; T44775
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berlet
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Chic
 A.; Ehrlich, S.D.; Emmerson, P.T.; Estlin, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gallet
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
 A:Authors: Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
 Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Roeha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akouch, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: C69973
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-91 <KUN>
 A:Cross-references: GB:299117; GB:AL009126; NID:g2634966; PIDN:CA14614.1; PID:g2635118
 A:Experimental source: strain 168
 R:Belitsky, B.R.; Gustafsson, M.C.U.; Sonenshein, A.L.; von Wachenfeldt, C.
 J. Bacteriol. 179, 5448-5457, 1997
 A:Title: An lrp-like gene of Bacillus subtilis involved in branched-chain amino acid tra
 A:Reference number: Z22837; MUID:97431495; PMID:9287000
 A:Accession: T44775
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-91 <BEL>
 A:Cross-references: EMBL:Y11043; NID:g1926275; PIDN:CA471938.1; PID:g1926279
 A:Experimental source: strain 1A1
 C:Genetics:
 A:Gene: yrdF
 C:Superfamily: Bacillus ribonuclease inhibitor

Query Match 100.0%; Score 20; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||

DB 34 NLDA 37

RESULT 18
 A55406
 calgranulin c - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 23-May-1997
 C:Accession: A55406
 R:Deil Angelica, E.C.; Schaeicher, C.H.; Santome, J.A.
 J. Biol. Chem. 269, 28929-28936, 1994
 A:Title: Primary structure and binding properties of calgranulin C, a novel S100-lik
 A:Reference number: A55406; MUID:95050708; PMID:7961855
 A:Accession: A55406
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-91
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand
 F:48-80/Domain: calmodulin repeat homology <ER2>

Query Match 100.0%; Score 20; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 59 NLDA 62

RESULT 19
 A97004
 barstar-like protein ribonuclease (barnase) inhibitor [imported] - Clostridium acetoi
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: A97004
 R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; I
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: A97004
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-91 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK78820.1; PID:g15023737; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0844

Query Match 100.0%; Score 20; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 34 NLDA 37

RESULT 20
 AB0449
 probable ribonuclease inhibitor YPO3690 [imported] - Yersinia pestis (strain C092)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AB0449
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, J
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0449
 A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-93 <KUR>
A:Cross-references: GB:AL590842; PIDN:GAC93158.1; PID:g15981608; GSPDB:GN00175
C:Genetics:
A:Gene: YPO3690

Query Match 100.0%; Score 20; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 34 NLDA 37

RESULT 21

A81176

ribonuclease inhibitor barstar NMB0646 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: A81176

R:Retellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Hatf, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: A81176

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <TEF>
A:Cross-references: GB:AE002419; GB:AE002098; NID:g7225863; PIDN:AAF41067.1; PID:g722587
A:Experimental source: serogroup B, strain MC58
C:Genetics: NMB0646

Query Match 100.0%; Score 20; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 33 NLDA 36

RESULT 22
A57483
3-mercaptopyruvate sulfotransferase (EC 2.8.1.2) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 19-Jan-2001
C:Accession: A57483

R:Nagahara, N.; Okazaki, T.; Nishino, T.
J. Biol. Chem. 270, 16230-16235, 1995
A:Title: Cytosolic mercaptopyruvate sulfotransferase is evolutionarily related to mitoc
vate sulfotransferase activity of rhodanese by site-directed mutagenesis.
A:Reference number: A57483; MUID:95332330; PMID:7608189
A:Accession: A57483

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-96 <NAG>
C:Superfamily: thiosulfate sulfotransferase
C:Keywords: sulfotransferase
F:77/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 100.0%; Score 20; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 1 NLDA 4

RESULT 23
C84003
exogenous DNA-binding protein comGC [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: C84003
R:Takami, H.; Nakasone, K.; Takaki, Y.; Meno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C84003

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <SNO>
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA06546.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics: comGC

Query Match 100.0%; Score 20; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 70 NLDA 73

RESULT 24
A85821
unknown protein encoded within prophage CP-933U [imported] - Escherichia coli (strain
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A85821
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85821

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <STO>
A:Cross-references: GB:AE005174; NID:g12515136; PIDN:AA657029.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3120

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 25
E90973
hypothetical protein Ecs2757 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: E90973
R:Haysht, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90973

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036180.1; PID:g13362225; GSPDB:GN00154

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 26
E90973
hypothetical protein Ecs2757 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: E90973
R:Haysht, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90973

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036180.1; PID:g13362225; GSPDB:GN00154

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 27
E90973
hypothetical protein Ecs2757 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: E90973
R:Haysht, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90973

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036180.1; PID:g13362225; GSPDB:GN00154

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 28
E90973
hypothetical protein Ecs2757 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: E90973
R:Haysht, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90973

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036180.1; PID:g13362225; GSPDB:GN00154

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||
Db 59 NLDA 62

RESULT 29
E90973
hypothetical protein Ecs2757 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: E90973
R:Haysht, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90973

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036180.1; PID:g13362225; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECS2757

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 59 NLDA 62

RESULT 26

E72664
hypothetical protein APE0740 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E72664
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakeyama, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, T.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72664
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <RAW>
A:Cross-references: DDBJ:AF000060; NID:95104188; PIDN:BA97971.1; PID:dl043503; PID:9510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0740

Query Match 100.0%; Score 20; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 43 NLDA 46

RESULT 27

S50356
sugar transport protein truncated homolog YIL171w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein Y19402.06A
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 19-Apr-2002
C:Accession: S50356
R:Lyle, G.; Bowman, S.; Churcher, C.
submitted to the EMBL Data Library, December 1994
A:Reference number: S50349
A:Accession: S50356
A:Molecule type: DNA
A:Residues: 1-109 <LVE>
A:Cross-references: GB:247047; EMBL:246921; GSPDB:GM00009; MIPS:YIL171w; NID:g603997; PI
C:Genetics:
A:Gene: SGD:HX112; MIPS:YIL171w
A:Cross-references: SGD:S0001433
A:Map position: 9L
C:Superfamily: maltose transport protein MAL61
C:Keywords: transmembrane protein
F:60-76/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 20; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 40 NLDA 43

RESULT 28

S65003
hypothetical protein YLR154c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein IJ341
C:Species: Saccharomyces cerevisiae
C:Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002
C:Accession: S65003; S6535
R:Reger, M.; Mueller-Auer, S.; Brueckner, M.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64987
A:Accession: S65003
A:Molecule type: DNA
A:Residues: 1-110 <RTD>
A:Cross-references: EMBL:Z73326; NID:g1360587; PIDN:CAA97726.1; PID:g1360588; MIPS:YL
A:Experimental source: strain S288C
R:van den Berg, M.A.; Steensma, H.Y.
Eur. J. Biochem. 231, 704-713, 1995
A:Title: ACS2, a Saccharomyces cerevisiae gene encoding acetyl-coenzyme A synthetase,
A:Reference number: S6534; MUID:95377302; PMID:7649171
A:Accession: S6535
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-110 <VAN>
A:Cross-references: EMBL:S79456; NID:g168013; PIDN:AAB35144.1; PID:g1683551
C:Genetics:
A:Cross-references: SGD:S0004144
A:Map position: 12R
A:Note: YLR154c
C:Superfamily: Saccharomyces hypothetical protein YLR154c

Query Match 100.0%; Score 20; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 7 NLDA 10

RESULT 29

A75544
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
C:Accession: A75544
R:Witte, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Yamchevyan, J.J.; Lam, P.; McDonald, L.; Oltetback, T.; Zalewski, C.;
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75544
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <WHI>
A:Cross-references: GB:AE001886; GB:AE00513; NID:g6457921; PIDN:AAF09825.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0242
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2705c

Query Match 100.0%; Score 20; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
|||||
DB 86 NLDA 89

RESULT 30

AG0725

conserved hypothetical protein SRY1952 [imported] - *Salmonella enterica* subsp. *enterica*
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A:Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 31-Dec-2001
 C:Accession: AG0725
 R:ParKhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov. A:Reference number: AB0502; PMID:11677608
 A:Accession: AG0725
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05505.1; PID:916503009; GSPDB:GN00176
 C:Genetics:
 A:Gene: SRY1952
 C:Superfamily: hypothetical protein HT0719

Query Match 100.0%; Score 20; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 30 NLDA 33

RESULT 31
 AF0252
 conserved hypothetical protein YPO2070 [imported] - *Yersinia pestis* (strain C092)
 C:Species: *Yersinia pestis*
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 01-Feb-2002
 C:Accession: AF0252
 R:ParKhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
 A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AF0252
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC90882.1; PID:915980081; GSPDB:GN00175
 C:Genetics:
 A:Gene: YPO2070
 C:Superfamily: hypothetical protein HT0719

Query Match 100.0%; Score 20; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 30 NLDA 33

RESULT 32
 H89785
 hypothetical protein [imported] - *Staphylococcus aureus* (strain N315)
 C:Species: *Staphylococcus aureus*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: H89785
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001
 C: Slib, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: AB9758; MUID:21311952; PMID:11418146
 A:Accession: H89785

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-114 <KUR>
 A:Cross-references: GB:BA000018; PID:913700144; PIDN:BA041443.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA0221

Query Match 100.0%; Score 20; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 63 NLDA 66

RESULT 33
 D32227
 hypothetical protein 4 (mer operon) - *Bacillus* sp.
 C:Species: *Bacillus* sp.
 C:Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #text_change 15-Oct-1999
 C:Accession: D32227
 R:Wang, Y.; Moore, M.; Levinson, H.S.; Silver, S.; Walsh, C.; Mahler, I.
 J. Bacteriol. 171, 83-92, 1989
 A:Title: Nucleotide sequence of a chromosomal mercury resistance determinant from a B. A:Reference number: A32227; MUID:8913092; PMID:2536669
 A:Accession: D32227
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115 <MAN>
 A:Cross-references: GB:M22708; NID:9143188; PIDN:AAA83976.1; PID:91129096

Query Match 100.0%; Score 20; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 99 NLDA 102

RESULT 34
 T44504
 merp protein [imported] - *Clostridium butyricum*
 C:Species: *Clostridium butyricum*
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
 C:Accession: T44504
 R:Narita, M.; Koizumi, T.; Huang, C.; Endo, G.
 Submitted to the EMBL data library, March 1999
 A:Description: Broad-spectrum mercury resistance and its genetic characterization of n. A:Reference number: 222785
 A:Accession: T44504
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-116 <NAK>
 A:Cross-references: EMBL:AB024961; PIDN:BAA86116.1
 A:Experimental source: isolate Mersaru
 C:Genetics:
 A:Gene: merp

Query Match 100.0%; Score 20; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 100 NLDA 103

RESULT 35
 T45512

probable transport protein orf4 [imported] - *Exiguobacterium* sp. plasmid pK1H3
 C:Species: *Exiguobacterium* sp.
 C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T45512
 R:Bogdanova, E.S.; Bass, I.A.; Minakhin, L.S.; Petrova, M.A.; Mindlin, S.Z.; Volodin, A.
 Microbiology 144, 609-620, 1998
 A:Title: Horizontal spread of mer operons among Gram-positive bacteria in natural enviro
 A:Reference number: 222993; MUID:98195721; PMID:9534232
 A:Accession: T45512
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-116 <R0G>
 A:Cross-references: EMBL:X99457; NID:93413183; PIDN:CAA67821.1; PID:93413187
 A:Experimental source: strain TC38-2b
 C:Genetics:
 A:Genome: plasmid pK1H3
 A:Note: ORF4
 A:Function:
 A:Description: may be involved in mercury resistance

Query Match 100.0%; Score 20; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 100 NIDA 103

RESULT 36
 C64562
 hypothetical protein HP0339 - *Helicobacter pylori* (strain 26695)
 C:Species: *Helicobacter pylori*
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: C64562
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 386, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: C64562
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-116 <TOM>
 A:Cross-references: GB:AE000551; GB:AE000511; NID:92313430; PIDN:AA07411.1; PID:9231344
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: phage T4 lysozyme homology
 F:4-109/Domain: phage T4 lysozyme homology <T4L>

Query Match 100.0%; Score 20; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 54 NIDA 57

RESULT 37
 F83714
 holo-[acyl carrier protein] synthase BH0518 [imported] - *Bacillus halodurans* (strain C-1
 C:Species: *Bacillus halodurans*
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: F83714
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: F83714
 A>Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-119 <STO>
 A:Cross-references: GB:AP001508; GB:BA000004; NID:q10172890; PIDN:BA04237.1; GSPDB:(
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0518
 C:Superfamily: holo-ACP synthase

Query Match 100.0%; Score 20; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 92 NIDA 95

RESULT 38
 S55326
 pseudozurin - *Thiosphaera pantotropha*
 N:Alternate names: blue copper protein
 C:Species: *Thiosphaera pantotropha*
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Apr-2000
 C:Accession: S55326
 R:Chan, C.; Willis, A.C.; Robinson, C.V.; Applin, R.T.; Radford, S.E.; Ferguson, S.J.
 Biochem. J. 308, 585-590, 1995
 A:Title: The complete amino acid sequence confirms the presence of pseudozurin in T)
 A:Reference number: S55326; MUID:95289994; PMID:7772045
 A:Accession: S55326
 A:Molecule type: protein
 A:Residues: 1-123 <CHA>
 C:Superfamily: plastocyanin
 C:Keywords: copper; electron transfer; metalloprotein
 F:1-123/Product: pseudozurin [status experimental <MAT>
 F:40,78,81,86/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 100.0%; Score 20; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 98 NIDA 101

RESULT 39
 C98286
 hypothetical protein AGR_L_2486 [imported] - *Agrobacterium tumefaciens* (strain C58, C
 C:Species: *Agrobacterium tumefaciens*
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
 C:Accession: C98286
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldm
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*
 A:Reference number: A97359; PMID:11743194
 A:Accession: C98286
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-125 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK9813.1; PID:q15159743; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR_L_2486
 A:Map position: linear chromosome

Query Match 100.0%; Score 20; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 74 NIDA 77

```
RESULT 40
S53340
CD59 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999
C:Accession: S53340; S53339
R:Rushmere, N.K.; Harrison, R.A.; van den Berg, C.W.; Morgan, B.P.
Biochem. J. 304, 595-601, 1994
A:Title: Molecular cloning of the rat analogue of human CD59: structural comparison with
A:Reference number: S53339; MUID:95091697; PMID:7528012
A:Accession: S53340
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <RUS>
A:Cross-references: GB:U48255; NID:g1199654; PIDN:AAA88909.1; PID:g1199655
A:Accession: S53339
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-24,'X',26-27,'X',29-34,'X',36-37,'X',39-40,'X',42-47,'X',49-58,'X',60,'X'
C:Superfamily: Ly-6 antigen; Ly-6 homology
F:23-101/Domain: Ly-6 homology <LY6>

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 126;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
Db 44 NLDA 47

RESULT 41
T18655
hypothetical protein B0035.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T18655
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19002
A:Accession: T18655
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-126 <MIL>
A:Cross-references: EMBL:Z73102; PIDN:CAA97410.1; GSPDB:GN00022; CESP:B0035.4
A:Experimental source: clone B0035
C:Genetics:
A:Gene: CESP:B0035.4
A:Map position: 4
A:Introns: 29/3; 73/3
C:Superfamily: Arabidopsis thaliana hypothetical protein F22013.29

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 126;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
Db 121 NLDA 124

RESULT 42
AH1425
hypothetical secreted protein lmo2809 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AH1425
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
```

```
ok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD01022.1; PID:g16412309; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2809

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 126;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
Db 53 NLDA 56

RESULT 43
AG1425
hypothetical secreted protein lmo2808 [imported] - Listeria monocytogenes (strain EGD
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG1425
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl,
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD01021.1; PID:g16412308; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2808

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 127;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
| | | |
Db 53 NLDA 56

RESULT 44
AE1933
hypothetical protein alr1016 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AE1933
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
DNA Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11758440
A:Accession: AE1933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072973.1; PID:g17130362; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1016
```

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2705c

Query Match 100.0%; Score 20; DB 2; Length 129;

Best Local Similarity 100.0%; Pred. NO. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

DB 101 NLDA 104

RESULT 45

AC0782

probable DNA-binding protein stry2429 [imported] - Salmonella enterica subsp. enterica se

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AC0782

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Conerton, P.; Croft, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; PMID:11677608

A:Accession: AC0782

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-129 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD02577.1; PID:G16503435; GSPDB:GN00176

C:Genetics:

A:Gene: STRY2429

Query Match 100.0%; Score 20; DB 2; Length 129;

Best Local Similarity 100.0%; Pred. NO. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4

DB 70 NLDA 73

Search completed: February 6, 2003, 11:23:12
Job time : 12.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 5.33333 Seconds
(without alignments)
31.107 Million cell updates/sec

Title: PAT943-6
Perfect score: 20
Sequence: 1 nlda 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 547

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	54	1 VG87_BPMD2	O64268 mycobacteri
2	20	100.0	70	1 RPKX_YEAST	P40422 saccharomyc
3	20	100.0	75	1 TRV3_ECOLI	P05835 escherichia
4	20	100.0	82	1 YN1L_FRAAL	P46041 frankia aln
5	20	100.0	85	1 GLR1_ECOLI	P00277 escherichia
6	20	100.0	89	1 BARS_BACAM	P11540 bacillus am
7	20	100.0	91	1 S112_PIG	P80310 sus scrofa
8	20	100.0	102	1 CMGC_BACHD	O96f96 homo sapien
9	20	100.0	103	1 S112_HUMAN	O96f96 homo sapien
10	20	100.0	109	1 Y1R1_YEAST	P40440 saccharomyc
11	20	100.0	114	1 Y0AB_ECOLI	P76258 escherichia
12	20	100.0	119	1 ACPS_BACHD	O96f91 bacillus ha
13	20	100.0	119	1 SY24_HUMAN	O00175 homo sapien
14	20	100.0	123	1 AZUP_PARDE	P80649 paracoccus
15	20	100.0	124	1 Y670_PASMU	O96my0 pasteurilla
16	20	100.0	126	1 CD59_RAT	P27274 rattus norv
17	20	100.0	126	1 PPD4_CAEEL	O17435 caenorhabdi
18	20	100.0	132	1 FL5A_PSEAE	O33422 pseudomonas
19	20	100.0	133	1 Y044_BORBU	O51073 borrellia bu
20	20	100.0	145	1 AZUP_PARP	P80401 paracoccus
21	20	100.0	150	1 SPOA_BACCE	P52930 bacillus ce
22	20	100.0	157	1 ISPE_LISIN	O96f39 listeria in
23	20	100.0	157	1 ISPE_LISIN	O96f39 listeria in
24	20	100.0	159	1 NIFX_RHOCA	P18078 rhodobacter
25	20	100.0	160	1 FLAV_CLOSA	P18855 clostridium
26	20	100.0	164	1 PHEA_SYNY1	P20778 synchocyst
27	20	100.0	168	1 NUE2_RHIME	P56910 rhizobium m
28	20	100.0	172	1 YFIR_ECOLI	O96f91 escherichia
29	20	100.0	176	1 YWY1_CAEEL	O11088 caenorhabdi
30	20	100.0	184	1 KAD1_AKNSP	O89p18 anaerobact
31	20	100.0	189	1 TBP_THECE	O56253 thebaccoc
32	20	100.0	190	1 TBP_PYROO	O52366 pyrococcus
33	20	100.0	191	1 SPOA_BACPU	P52933 bacillus pu

34	20	100.0	191	1 TXLA_SYNP7	P35088 synchococc
35	20	100.0	195	1 IND1_HUMAN	P37290 homo sapien
36	20	100.0	197	1 YDB6_YEAST	O12055 saccharomyc
37	20	100.0	202	1 GD1R_YEAST	O12434 saccharomyc
38	20	100.0	207	1 COAE_XYLF	O96p12 xyella fas
39	20	100.0	209	1 VS10_ROTBS	P34718 bovine rota
40	20	100.0	210	1 SPOA_BACCI	P52931 bacillus ci
41	20	100.0	210	1 VS10_ROTTC	P36358 porcine rot
42	20	100.0	211	1 SODE_ACIAM	O96p13 acidilanus a
43	20	100.0	212	1 IL6_CERTO	P46650 cercocebus
44	20	100.0	212	1 IL6_HUMAN	P05231 homo sapien
45	20	100.0	212	1 IL6_MACFA	P79341 macaca fasc

ALIGNMENTS

RESULT 1					
VG87_BPMD2	STANDARD:	PRT:	54 AA.		
ID VG87_BPMD2					
AC O64268;					
DT 15-DEC-1998 (Rel. 37, Created)					
DT 15-DEC-1998 (Rel. 37, Last sequence update)					
DT 15-DEC-1998 (Rel. 37, Last annotation update)					
DE Gene 87 protein (GP87).					
GN 87.					
OS Mycobacteriophage D29.					
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;					
OC unclassified Siphoviridae.					
OX NCBI_TaxID=28369;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=98300335; PubMed=9636706;					
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;					
RT "Genome structure of mycobacteriophage D29: implications for phage evolution.";					
RT J. Mol. Biol. 279:143-164(1998).					
RL					
CC					
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CC					
DR EMBL: AF022214; AACI8517.1;					
SO SEQUENCE 54 AA; 6210 MW; C6D36552F48CE621 CRC64;					
Query Match					
Best Local Similarity	100.08;	Score 20;	DB 1;	Length 54;	
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 N LDA 4				
DB	9 N LDA 12				
RESULT 2					
RPCK_YEAST					
ID RPKX_YEAST	STANDARD:	PRT:	70 AA.		
AC P40422;					
DT 01-FEB-1995 (Rel. 31, Created)					
DT 01-FEB-1995 (Rel. 31, Last sequence update)					
DT 15-JUL-1999 (Rel. 38, Last annotation update)					
DE DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide					
DE (EC 2.7.7.6) (ABC10-alpha).					
GN RPO10 OR RPB12 OR YHR143BW.					
OS Saccharomyces cerevisiae (Baker's yeast).					
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;					
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.					
OX NCBI_TaxID=4932;					
RN [1]					

```

OS      Escherichia coli.
OC      Plasmid IncfII R100-1, and plasmid IncfII R100.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      PLASMID-IncfII R100-1;
RX      MEDLINE=87008371; PubMed=3531163;
RA      Inamoto S., Yoshioaka Y., Ohtsubo E.;
RT      "Identification and characterization of the products from the traJ
RT      and traY genes of plasmid R100.";
RL      J. Bacteriol. 170:2749-2757(1988);
CC      -I- FUNCTION: INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS
CC      FOR THE EXCHANGE OF PLASMID DNA. IT IS ALSO RESPONSIBLE FOR
CC      CONUGAL DNA METABOLISM. TRAY IS REQUIRED FOR STRAND-SPECIFIC
CC      NICKING AT ORIT, THE TRANSFER ORIGIN.
CC      -I- SIMILARITY: TO TRAY PROTEIN OF OTHER PLASMIDS.
CC      -----
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CC      or send an email to license@sdb.ch).
CC      -----
DR      EMBL; M15136; AAA26076.1; -.
DR      EMBL; M20941; AAA26073.1; -.
DR      PIR; C35033; BVECRY.
DR      PIR; C32014; C32014.
SQ      Plasmid; conjugation; DNA-binding
KW      SEQUENCE 75 AA; 8542 MW; 88D4D04C4B5DE07A CRC64;

Query Match      100.0%; Score 20; DB 1; Length 75;
Best Local Similarity 100.0%; Predl No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NDA 4
      ||||
DB      57 NDA 60

RESULT 4
ID      YNII_FRAAL
ID      YNII_FRAAL STANDARD; PRT; 82 AA.
AC      P46041;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical 9.1 kDa protein in nifH-nifW intergenic region (ORF1).
OS      Frankia alni.
OC      Bacteria; Actinobacteria; Actinobacteridae;
OC      Actinomycetales; Frankineae; Frankiaceae; Frankia.
OX      NCBI_TaxID=1859;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Cp11;
RX      MEDLINE=95369734; PubMed=7642138;
RA      Harriott O.T., Hosted T.J., Benson D.R.;
RT      "Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia
RT      nitrogen fixation gene cluster.";
RL      Gene 161:63-67(1995).
CC      -I- SIMILARITY: TO SIMILAR PROTEINS IN OTHER NITROGEN-FIXING BACTERIA

```

THIS PROTEIN IS GENERALLY FOUND IN THE NIFX-NIFW INTERGENIC REGION
OR IN THE FIXX 3' REGION.

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 CC EMBL: L29299; AAC82972.1; -
 CC DR Hypothetical protein; Nitrogen fixation.
 CC KM SEQUENCE 82 AA; 9081 MW; AFBBD86827B4322C CRC64;
 CC

Query Match 100.0%; Score 20; DB 1; Length 82;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 Db 17 NIDA 20

RESULT 5
 ID GLRL_ECOLI STANDARD; PRT; 85 AA.
 AC P00277;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE glutaredoxin 1 (grx1).
 GN GRX1 OR GRX OR B0849.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87005940; PubMed=3530878;
 RA Hoeeg J.-O., von Bahr-Lindstrom H., Joernvall H., Holmgren A.;
 RT "Cloning and expression of the glutaredoxin (grx) gene of Escherichia
 RT coli.";
 RL Gene 43:13-21(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chatterjee P.K., Sternberg N.L.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RT Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Iton T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino S., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sasaki G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RT DNA Res. 3:137-155(1996).
 RN [5]
 RP SEQUENCE.

RC STRAIN=K12;
 RX MEDLINE=84004402; PubMed=6352262;
 RA Hoeeg J.-O., Joernvall H., Holmgren A., Carlquist M., Persson M.;
 RT "The primary structure of Escherichia coli glutaredoxin. Distant
 RT homology with thioredoxins in a superfamily of small proteins with a
 RT redox-active cysteine disulfide/cysteine dithiol.";
 RL Eur. J. Biochem. 136:223-232(1983).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=91364685; PubMed=1889405;
 RA Sodano P., Charly K.V.R., Bjoernberg O., Holmgren A., Kren B.,
 RA Fuchs J.A., Wuehrich K.;
 RT "Nuclear magnetic resonance studies of recombinant Escherichia coli
 RT glutaredoxin. Sequence-specific assignments and secondary structure
 RT determination of the oxidized form.";
 RL Eur. J. Biochem. 200:369-377(1991).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=92046066; PubMed=1942053;
 RA Sodano P., Xia T.-H., Bushweller J.H., Bjoernberg O., Holmgren A.,
 RA Billeter M., Wuehrich K.;
 RT "Sequence-specific 1H NMR assignments and determination of the three-
 RT dimensional structure of reduced Escherichia coli glutaredoxin.";
 RL J. Mol. Biol. 221:1311-1324(1991).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93278264; PubMed=1304339;
 RA Xia T.-H., Bushweller J.H., Sodano P., Billeter M., Bjoernberg O.,
 RA Holmgren A., Wuehrich K.;
 RT "NMR structure of oxidized Escherichia coli glutaredoxin: comparison
 RT with reduced E. coli glutaredoxin and functionally related
 RT proteins.";
 RL Protein Sci. 1:310-321(1992).
 RN [9]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97270442; PubMed=9125525;
 RA Kelley J.J. III, Caputo M., Eaton S.F., Laue T.M., Bushweller J.H.;
 RT "Comparison of backbone dynamics of reduced and oxidized Escherichia
 RT coli glutaredoxin-1 using 15N NMR relaxation measurements.";
 RL Biochemistry 36:5029-5044(1997).
 CC -1- FUNCTION: THE DISULFIDE BOND FUNCTIONS AS AN ELECTRON CARRIER IN
 CC THE GLUTATHIONE-DEPENDENT SYNTHESIS OF DEOXYRIBONUCLEOTIDES BY THE
 CC ENZYME RIBONUCLEOTIDE REDUCTASE. IN ADDITION, IT IS ALSO INVOLVED
 CC IN REDUCING SOME DISULFIDES IN A COUPLED SYSTEM WITH GLUTATHIONE
 CC REDUCTASE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAREDOXIN FAMILY.
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 CC EMBL: M13449; AAA23936.1; -
 CC EMBL: U18655; AAC43449.1; -
 CC EMBL: AE000187; AAC73936.1; -
 CC EMBL: D90722; BAA35552.1; -
 CC EMBL: D90723; BAA35560.1; -
 CC PIR: A00283; GDEC.
 CC PDB: 1EG0; 31-OCT-93.
 CC PDB: 1EGR; 31-OCT-93.
 CC PDB: 1GRX; 24-JUN-98.
 CC EC02DBASE: B011.0; 6TH EDITION.
 CC EcoGene: EG10417; grxa.
 CC InterPro: IPR002103; Glutaredoxin.
 CC Pfam: PF00462; glutaredoxin; 1.
 CC PRINTS: PR00160; GLUTAREDOXIN.
 CC PROSITE: PS00195; GLUTAREDOXIN; 1.
 CC Redox-active center; Electron transport; 3D-structure;
 CC Deoxyribonucleotide synthesis; Complete proteome.

```

FT DISULFID 11 14 REDOX-ACTIVE.
SQ SEQUENCE 85 AA; 9685 MW; 33C185A47021EF42 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 85;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
   ||||
DB 82 NLDA 85

RESULT 6
BARS_BACAM STANDARD; PRT; 89 AA.
AC P11540;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Barstar (Ribonuclease inhibitor).
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1390;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89012012; PubMed=3050134;
RA Hartley R.W.;
RT "Barnase and barstar. Expression of its cloned inhibitor permits
   expression of a cloned ribonuclease."
RL J. Mol. Biol. 202:913-915(1988).
RN [2]
RP REVIEW.
RX MEDLINE=90162921; PubMed=2696173;
RA Hartley R.W.;
RT "Barnase and barstar: two small proteins to fold and fit together."
RL Trends Biochem. Sci. 14:450-454(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH BARNASE.
RA Guillet V., Lapphorn A., Hartley R.W., Mauguen Y.;
RT "Recognition between a bacterial ribonuclease, barnase, and its
   natural inhibitor, barstar."
RL Structure 1:165-177(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF COMPLEX WITH RNASE SA.
RX MEDLINE=98437624; PubMed=9757110;
RA Sevik J., Urbanikova L., Dauter Z., Wilson K.S.;
RT "Recognition of RNase Sa by the inhibitor barstar: structure of the
   complex at 1.7 A resolution."
RL Acta Crystallogr. D 54:954-963(1998).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=94009694; PubMed=8405454;
RA Lubienki M.J., Bycroft M., Jones D.N.M., Fersht A.R.;
RT "Assignment of the backbone 1H and 15N NMR resonances and secondary
   structure characterization of Barstar."
RL FEBS Lett. 332:81-87(1993).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE=94318630; PubMed=8043574;
RA Lubienki M.J., Bycroft M., Freund S.M.V., Fersht A.R.;
RT "Three-dimensional solution structure and 13C assignments of barstar
   using nuclear magnetic resonance spectroscopy."
RL Biochemistry 33:8866-8877(1994).
CC -1- FUNCTION: INHIBITOR OF THE RIBONUCLEASE BARNASE. FORMS A ONE-TO-
   ONE NON-COVALENT COMPLEX.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -----
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CC -----
DR EMBL: X15545; CA33551.1; -.
DR F1R; S01373; S01373.
DR PDB; 1BRS; 31-JUL-94.
DR PDB; 1B7A; 31-JUL-94.
DR PDB; 1B7B; 31-JUL-94.
DR PDB; 1A87; 04-SEP-97.
DR PDB; 1A87; 04-SEP-97.
DR PDB; 1A19; 08-APR-98.
DR PDB; 1B27; 09-DEC-98.
DR PDB; 1B25; 09-DEC-98.
DR PDB; 1B2U; 09-DEC-98.
DR PDB; 1B3S; 09-DEC-98.
DR PDB; 1A7Y; 02-MAR-99.
DR InterPro; IPR000468; Barstar.
DR Pfam; PF01337; Barstar; 1.
DR ProDom; PD029050; Barstar; 1.
KW 3D-structure.
FT INIT MET 0
SQ SEQUENCE 89 AA; 10212 MW; 3AC7E76A9C43A505 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
   ||||
DB 33 NLDA 36

RESULT 7
S112_PIG STANDARD; PRT; 91 AA.
AC P80310;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calgranulin C (CAGC).
GN S100A12.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP TISSUE=granulocyte;
RC MEDLINE=95050708; PubMed=7961855;
RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
RT "Primary structure and binding properties of calgranulin C, a novel
   S100-like calcium-binding protein from pig granulocytes."
RL J. Biol. Chem. 269:28929-28936(1994).
CC -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL
   AMOUNTS FOUND IN LYMPHOCYTES.
CC -1- MISCELLANEOUS: IN THE ABSENCE OF ZINC BINDS ONE CALCIUM ION PER
   MOLECULE.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND [CALCIUM-BINDING DOMAINS.
   MOLECULE.
CC HSP; P80511; 1E8A.
DR InterPro; IPR001751; CABP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR ProDom; PD003407; CABP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; zinc; Metal-binding.
FT CA_BIND 18 31 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
FT CA_BIND 61 72 EF-HAND 2 (HIGH AFFINITY) (BY
   SIMILARITY).
SQ SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;

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Query Match 100.0%; Score 20; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 59 NLDA 62

RESULT 8
 CMGC_BACHD STANDARD; PRT; 102 AA.
 ID CMGC_BACHD
 AC 09K923;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Comg operon protein 3 homolog precursor.
 GN COMG OR BH2827.
 OS Bacillus halodurans.
 OC Bacillus; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=86655;
 OX NCBI_TaxID=86655;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE=20512582; Pubmed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhnra S.,
 RA Horikoshi K.;
 RT Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: REQUIRED FOR TRANSFORMATION AND DNA-BINDING (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
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 CC -----
 CC EMBL: AP001516; BAH06546.1; -
 DR InterPro: IPR000983; Bac_GSPG.
 DR InterPro: IPR002416; Bac_GSPH.
 DR InterPro: IPR001120; Prok_N_methyltn.
 DR PRINTS: PR00813; BCTERIALGSPG.
 DR PRINTS: PR00885; BCTERIALGSPH.
 DR PROSITE: PS00409; PROKAR_NTER_METHYL. 1.
 KM Transprot: Methylation; Transmembrane; Complete proteome.
 FT PROPP 1 10
 FT CHAIN 11 102
 FT TRANSMEM 11 31
 FT MOD_RES 11 11
 FT DISULFID 46 85
 FT SEQUENCE 102 AA; 11368 MW; 3C4BD89B08564A43 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 70 NLDA 73

RESULT 9
 ID S112_HUMAN STANDARD; PRT; 103 AA.
 AC 096F06;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Putative S100 calcium-binding protein MCG17528.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Cervix;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 CC EMBL: BC010541; AAH10541.1; -
 DR EMBL: BC019099; AAH19099.1; -
 DR InterPro: IPR001751; CABP_S100.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand. 1.
 DR Prodom: PD003407; S100_CABP; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 KM Hypothetical protein; Calcium-binding.
 FT CA_BIND 23 36
 FT CA_BIND 67 78
 FT SEQUENCE 103 AA; 11801 MW; 7D00C08F85697A6C CRC64;

Query Match 100.0%; Score 20; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 65 NLDA 68

RESULT 10
 ID Y1R1_YEAST STANDARD; PRT; 109 AA.
 AC P40440;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 11.6 kDa protein in SDL1 5' region.
 GN Y1171W OR Y19402.06A.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288c / AB972;
 RA Barrall B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Gentles S., Hamlyn N., Horneill T.S., Hunt S., Jagsels K., Jones W.,
 RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
 RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLE GLUCOSE TRANSPORTER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 CC -1- CAUTION: Y1171W AND Y1170W REPRESENT THE N- AND C-TERMINAL
 CC OF A PUTATIVE TRANSPORTER.
 CC -----

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CC -----
 CC EMBL: Z46881; CAA87021.1; -
 CC SGD: S0001432; HXT12.
 CC InterPro: IPR003662; sub_transporter.
 CC Pfam: PF00083; sugar_tr; 1.
 CC Hypothetical protein; Repeat; Transmembrane; Sugar transport;
 CC Transport; Glycoprotein.
 CC DOMAIN 1 56 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 57 77 POTENTIAL.
 CC DOMAIN 78 109 EXTRACELLULAR (POTENTIAL).
 CC CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 109 AA; 11638 MW; B9316C3626558434 CRC64;

Query Match Best Local Similarity 100.0%; Score 20; DB 1; Length 109;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 40 NLDA 43

RESULT 11
 YOB_ECOLI STANDARD; PRT; 114 AA.
 AC P76258;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yob.
 GN YOB OR B1809.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-97251358; PubMed-9097040;
 RT Iton T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
 RA Mizubuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
 RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
 RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
 RA Yamamoto Y., Horuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 CC -1- SIMILARITY: BELONGS TO THE UPF0076 (UK114) FAMILY.
 CC -----
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CC -----
 CC EMBL: AE000275; AAC74879.1; ALT_INIT.
 CC EMBL: D90825; BAA15618.1; ALT_INIT.
 CC HSSP: P37552; 10D9.
 CC EcoGene: EG13514; yob.
 CC InterPro: IPR000543; YyGF-like.
 CC Pfam: PF01042; UPF0076.1.
 CC PROSITE: PS01094; UPF0076.1.
 CC Hypothetical protein; Complete proteome.
 CC SEQUENCE 114 AA; 12493 MW; CB276C49F32AB754 CRC64;

Query Match Best Local Similarity 100.0%; Score 20; DB 1; Length 114;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 30 NLDA 33

RESULT 12
 ACPS_BACHD STANDARD; PRT; 119 AA.
 ID ACPS_BACHD
 AC O9KFG1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN ACPS OR BH0518.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=86665;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE-20512582; PubMed-11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kunara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE P-PANT TRANSFERASE SUPERFAMILY. ACPS
 CC FAMILY.
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CC -----
 CC EMBL: AP001508; BAB04237.1; -
 CC InterPro: IPR002582; ACPS.
 CC InterPro: IPR004568; Pantethn-trn.
 CC Pfam: PF01648; ACPS; 1.
 CC PRODOM: PD004282; ACPS; 1.
 CC TIGRFAMs: TIGR00516; acps; 1.
 CC TIGRFAMs: TIGR00556; pantethn-trn; 1.
 CC Transferase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
 CC Complete proteome.
 CC METAL 8 8 MAGNESIUM (BY SIMILARITY).
 CC METAL 58 58 MAGNESIUM (BY SIMILARITY).
 CC SEQUENCE 119 AA; 13421 MW; 2279E552549041C9 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 92 NLDA 95

RESULT 13
 SY24_HUMAN STANDARD; PRT; 119 AA.
 AC 000175;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A24 precursor (CCL24) (Myeloid progenitor
 DE Inhibitory factor-2) (MPF-2) (CK-beta-6) (Eotaxin-2).
 GN SCYA24 OR MPF2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-41 AND 73.
 RC TISSUE=Monocytes;
 RX MEDLINE=97258609; PubMed=9104803;
 RA Patel V.P., Kreider B.L., Li Y., Li H., Leung K., Salcedo T.,
 RA Nardelli B., Pipalla V., Gentz S., Thotakura R., Parmelee D.,
 RA Gentz R., Garotta G.;
 RT "Molecular and functional characterization of two novel human C-C
 RT chemokines as inhibitors of two distinct classes of myeloid
 RT progenitors";
 RL J. Exp. Med. 185:1163-1172(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
 RC TISSUE=Monocytes;
 RX MEDLINE=98030404; PubMed=9365122;
 RA White J.R., Imburgia C., Dul E., Appelbaum E., O'Donnell K.,
 RA O'Shannessy D.J., Bravner M., Fornwald J., Adamou J.,
 RA Elshourbagy N.A., Kaiser K., Foley J.J., Schmidt D.B., Johanson K.,
 RA Macphee C., Moores K., McNulty D., Scott G.F., Schleimer R.P.,
 RA Sarau H.M.;
 RT "Cloning and functional characterization of a novel human CC chemokine
 RT that binds to the CCR3 receptor and activates human eosinophils";
 RL J. Leukoc. Biol. 62:667-675(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Jones K., Graves T., Duckels G., Fronick W.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 3-117 FROM N.A.
 RA Hein H., Theran L.;
 RT "cDNA, genomic organisation and chromosomal location of the MPF-2
 RT (eotaxin-2) gene";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP STRUCTURE BY NMR.
 RX MEDLINE=20374512; PubMed=10913244;
 RA Mayer K.L., Stone M.J.;
 RT "NMR solution structure and receptor peptide binding of the CC
 RT chemokine eotaxin-2";
 RL Biochemistry 39:8382-8395(2000).
 CC -1- FUNCTION: CHEMOTACTIC FOR RESTING T LYMPHOCYTES, AND EOSINOPHILS.
 CC HAS LOWER CHEMOTACTIC ACTIVITY FOR NEUTROPHILS BUT NONE FOR
 CC MONOCYTES AND ACTIVATED LYMPHOCYTES. IS A STRONG SUPPRESSOR OF
 CC COLONY FORMATION BY A MULTIPOTENTIAL HEMATOPOIETIC PROGENITOR CELL
 CC LINE. BINDS TO CCR3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: ACTIVATED MONOCYTES AND ACTIVATED T
 CC LYMPHOCYTES.
 CC -1- PTM: N-GLYCOSYLATED.

CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
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 CC -----
 DR EMBL; U85768; AAB51135.1; -;
 DR EMBL; AC0005102; AAD15410.1; -;
 DR EMBL; AJ223461; CA11383.1; -;
 DR PDB; 1E1G; 06-DEC-00.
 DR PDB; 1E1H; 06-DEC-00.
 DR Genew; HGNC:10623; SCYA24.
 DR InterPro; IPR000827; CC_chemkine_sml.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00189; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; FALSE_NEG.
 DR Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response;
 KW 3D-structure.
 FT SIGNAL 1 26
 FT CHARIN 27 119
 FT DISULFID 33 58
 FT DISULFID 34 74
 FT CARBOHYD 115 115
 FT CONFLICT 61 61
 FT CONFLICT 73 73
 FT CONFLICT 73 73
 SO SEQUENCE 119 AA; 13133 MW; 6CAAC61731FB93 CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NLDA 4
 Db 88 NLDA 91
 RESULT 14
 AZUP_PARDE STANDARD; PRT; 123 AA.
 ID AZUP_PARDE
 AC P80649;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Pseudodazurin.
 OS Paracoccus denitrificans.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Paracoccus.
 OX NCBI_TaxID=266;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 8944;
 RX MEDLINE=97184655; PubMed=9032456;
 RA Leung Y.-C., Chan C., Reader J.S., Willis A.C., van Spanning R.J.M.,
 RA Ferguson S.J., Radford S.E.;
 RT "The pseudodazurin gene from Pseudomonas panotrophica: analysis of
 RT upstream putative regulatory sequences and overexpression in
 RT Escherichia coli";
 RL Biochem. J. 321:699-705(1997).
 CC -1- FUNCTION: THIS SOLUBLE ELECTRON TRANSFER COPPER PROTEIN IS
 CC REQUIRED FOR THE INACTIVATION OF COPPER-CONTAINING NITRITE
 CC REDUCTASE IN THE PRESENCE OF OXYGEN.
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
 CC HSP; P80401; IADW.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR001235; Copper_blue.
 DR Pfam; PF00127; copper_bind_1.

DR PRINTS: PR00156; COPPERBLUE.
DR PRODOM: PD001235; COPPER.BLUE; 1.
DR PROSITE: PS00196; COPPER.BLUE; 1.
KM Copper: Electron transport; Periplasmic.
FT DOMAIN 5 93 PLASTOCYANIN-LIKE.
FT METAL 40 40 COPPER (BY SIMILARITY).
FT METAL 78 78 COPPER (BY SIMILARITY).
FT METAL 81 81 COPPER (BY SIMILARITY).
FT METAL 86 86 COPPER (BY SIMILARITY).
SQ SEQUENCE 123 AA; 13337 MW; 983800FBB5589E2 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 98 NLDA 101

RESULT 15
Y670_PASMU
ID Y670_PASMU STANDARD; PRT: 124 AA.
AC O9CMY0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein PM0670 precursor.
GN PM0670.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-Pm70;
RX MEDLINE=21145866; Pubmed=11248100;
RA May B.J., Zhang Q., Li L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B562 FAMILY.
CC
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CC
CC EMBL: AE006103; AKK02754.1; -
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 124 HYPOTHETICAL PROTEIN PM0670.
SQ SEQUENCE 124 AA; 13746 MW; D7B2B485C7B51B9A CRC64;

Query Match 100.0%; Score 20; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 101 NLDA 104

RESULT 16
CD59_RAT
ID CD59_RAT STANDARD; PRT: 126 AA.
AC P27274;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition

DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN CD59.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-64.
RC STRAIN-Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95091697; Pubmed=7528012;
RA Rushmere N.K., Harrison R.A., van den Berg C.W., Morgan B.P.;
RT "Molecular cloning of the rat analogue of human CD59: structural
RT comparison with human CD59 and identification of a putative active
RT site.";
RL Biochem. J. 304:595-601(1994).
RN [2]
RP SEQUENCE OF 23-37.
RC TISSUE=Erythrocyte;
RX MEDLINE=92286999; Pubmed=1376109;
RA Hughes T.R., Piddlesden S.J., Williams J.D., Harrison R.A.,
RA Morgan B.P.;
RT "Isolation and characterization of a membrane protein from rat
RT erythrocytes which inhibits lysis by the membrane attack complex of
RT rat complement.";
RL Biochem. J. 284:169-176(1992).
CC -1- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
CC COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C5B-8 STAGE OF MAC
CC ASSEMBLY.
CC
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC
CC -1- PTM: N-GLYCOSYLATED.
CC
CC -1- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
CC
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CC
CC EMBL: U48255; AA88909.1; -
DR HSSP: P13987; ICDS.
DR InterPro: IPR001526; LY6_UPAR.
DR InterPro: IPR003632; LY-6_CD59.
DR Pfam: PF00021; UPAR_LY6; 1.
DR PRODOM: PD003128; LY-6_CD59; 1.
DR SMART: SM00134; LY; 1.
DR PROSITE: PS00983; LY6_UPAR; 1.
KW Antigen; Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 22
FT CHAIN 23 101 CD59 GLYCOPROTEIN.
FT PROPEP 102 126 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 101 101 GPI-ANCHOR (BY SIMILARITY).
FT DOMAIN 23 110 UPAR/LY6.
FT DISULFID 25 48 BY SIMILARITY.
FT DISULFID 28 35 BY SIMILARITY.
FT DISULFID 41 61 BY SIMILARITY.
FT DISULFID 67 85 BY SIMILARITY.
FT DISULFID 86 91 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 126 AA; 13790 MW; 54B9C58AB2073005 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 44 NLDA 47

RESULT 17
PFDA_CAREL

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ID  PFD4_CAEEL  STANDARD;  PRT;  126 AA.
AC  017435:
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DE  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Probable prefoldin subunit 4.
GN  B0035.4.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Pelodierinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-Bristol N2;
RA  White S.;
RL  Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-Bristol N2;
RA  Kohara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M.,
RA  Thierry-Mieg Y., Thierry-Mieg D., Thierry-Mieg J.;
RA  Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC  -1- FUNCTION: BINDS SPECIFICALLY TO CYTOSOLIC CHAPERONIN (C-CPN) AND
CC  TRANSFERS TARGET PROTEINS TO IT. BINDS TO NASCENT POLYPEPTIDE
CC  CHAIN AND PROMOTES FOLDING IN AN ENVIRONMENT IN WHICH THERE ARE
CC  MANY COMPETING PATHWAYS FOR NONNATIVE PROTEINS (BY SIMILARITY).
CC  -1- SUBUNIT: HETEROHEXAMER OF TWO PRD-ALPHA TYPE AND FOUR PRD-BETA
CC  TYPE SUBUNITS (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE PREFOLDIN BETA SUBUNIT FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: 273102; CA97410.1; -
DR  EMBL: AF292051; AAC41147.1; -
DR  WormPep: B0035.4; CE05162.
KW  Chaperone.
SQ  SEQUENCE 126 AA; 14031 MW; 22DBB5B370AB4DE8 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 121 NLDA 124

RESULT 18
FLSA_PSEAE STANDARD; PRT; 132 AA.
AC 033422:
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE A-type flagellar protein flis.
GN FLIS.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-98147712; PubMed-9488388;
RA Aroa S.K., Ritchings B.W., Almira E.C., Lory S., Ramphal R.;
RT "The Pseudomonas aeruginosa flagellar cap protein, Flid, is
RT responsible for mucin adhesion.";
```

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RL Infect. Immun. 66:1000-1007 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PAK, PA103, CS2, and CS32;
RX MEDLINE=20143761; PubMed=10678962;
RA Aroa S.K., Dasgupta N., Lory S., Ramphal R.;
RT "Identification of two distinct types of flagellar cap proteins, Flid,
RT in Pseudomonas aeruginosa.";
RL Infect. Immun. 68:1474-1479 (2000).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SIMILARITY: BELONGS TO THE FLIS FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L81176; AAC09392.1; -
DR EMBL: AF139822; AAF35978.1; -
DR EMBL: AF139823; AAF35980.1; -
DR EMBL: AF139824; AAF35982.1; -
DR EMBL: AF139825; AAF35984.1; -
DR InterPro: IPR003713; FLIS.
DR Pfam: PF02561; FLIS; 1.
DR TIGRfams: TIGR00208; flis; 1.
KW flagella.
SQ SEQUENCE 132 AA; 14250 MW; B8BC95E1890533D3 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
Db 78 NLDA 81
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RESULT 19
Y044_BORBU STANDARD; PRT; 133 AA.
AC 051073:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein BB0044.
GN BB0044.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kertavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt J., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uitterback T., Matthey L., McDonald L., Artlach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586 (1997).
CC -----
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DR EMBL; AE001118; AAC66442.1; -
DR TIGR; B80044; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSEM 11 31 POTENTIAL.
SQ SEQUENCE 133 AA; 16052 MW; A57686EA30F1959B CRC64;

Query Match 100.0%; Score 20; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 44 NLDA 47

RESULT 20
AZUP_PARPEN STANDARD; PRT; 145 AA.
ID AZUP_PARPEN
AC P80401;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pseudazurin precursor.
GN PAZS.
OS Paracoccus pantotrophus (Thiosphaera pantotropha).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Paracoccus.
OX NCBI_TaxID=82367;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-32.
RC STRAIN-ATCC 35512 / LMD 82.5;
RX MEDLINE=97184655; PubMed=9032456;
RA Leung Y.-C., Chan C., Reader J.S., Willis A.C., van Spanning R.J.M.,
RA Ferguson S.J., Radford S.E.;
RT "The pseudazurin gene from Thiosphaera pantotropha: analysis of
RT upstream putative regulatory sequences and overexpression in
RT Escherichia coli.";
RL Biochem. J. 321:699-705(1997).
RN [2]
RP SEQUENCE OF 23-145.
RC STRAIN-ATCC 35512 / LMD 82.5;
RX MEDLINE=95289994; PubMed=7772045;
RA Chan C., Willis A.C., Robinson C.V., Apelin R.T., Radford S.E.,
RA Ferguson S.J.;
RT "The complete amino acid sequence confirms the presence of
RT pseudazurin in Thiosphaera pantotropha.";
RL Biochem. J. 308:585-590(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA Williams P.A.;
RT Submitted (FEB-1997) to the PDB data bank.
CC -I- FUNCTION: THIS SOLUBLE ELECTRON TRANSFER COPPER PROTEIN IS
CC REQUIRED FOR THE INACTIVATION OF COPPER-CONTAINING NITRITE
CC REDUCTASE IN THE PRESENCE OF OXYGEN.
CC -I- SUBUNIT: HOMODIMER.
CC -I- SUBCELLULAR LOCATION: Periplasmic.
CC -I- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC
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DR EMBL; 273141; CAA97485.1; -
DR EMBL; 270033; CAA93848.1; -
DR PDB; 1ADW; 15-MAY-97.
DR InterPro; IPR000923; BlueCu_1.

DR InterPro; IPR001235; Copper_blue.
DR Pfam; PF00127; copper_bind_1.
DR PRINTS; PR00156; COPPERBLUE.
DR PRODOM; PD001235; Copper_blue; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
KW Copper; Electron transport; Signal; Periplasmic; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 145 PSEUDAZURIN.
FT DOMAIN 27 115 PLASTOCYANIN-LIKE.
FT METAL 62 62 COPPER (BY SIMILARITY).
FT METAL 100 100 COPPER (BY SIMILARITY).
FT METAL 103 103 COPPER (BY SIMILARITY).
FT METAL 108 108 COPPER (BY SIMILARITY).
SQ SEQUENCE 145 AA; 15446 MW; 725ECB5929EC3831 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 120 NLDA 123

RESULT 21
SPOA_BACCE STANDARD; PRT; 150 AA.
ID SPOA_BACCE
AC P52930;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stage 0 sporulation protein A (Fragment).
GN SPOOA.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NRRL 569;
RX MEDLINE=95191392; PubMed=7865226;
RA Brown D.P., Ganova-Raeva L., Green B.D., Wilkinson S.R., Young M.,
RA Youngman P.;
RT "Characterization of spoOA homologues in diverse Bacillus and
RT Clostridium species identifies a probable DNA-binding domain.";
RL Mol. Microbiol. 14:411-426(1994).
RN [1]
RP -I- FUNCTION: MAY PLAY THE CENTRAL REGULATORY ROLE IN SPOULATION. IT
CC MAY BE AN ELEMENT OF THE EFFECTOR PATHWAY RESPONSIBLE FOR THE
CC ACTIVATION OF SPOULATION GENES IN RESPONSE TO NUTRITIONAL STRESS.
CC SPOOA MAY ACT IN CONCERT WITH SPOOH (A SIGMA FACTOR) TO CONTROL
CC THE EXPRESSION OF SOME GENES THAT ARE CRITICAL TO THE SPOULATION
CC PROCESS. REPRESSOR OF ABRB. ACTIVATOR OF THE SPOOA OPERON. BINDS
CC THE DNA SEQUENCE 5'-TGCGAA-3' (OA BOX) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -I- PTM: PHOSPHORYLATED BY KINA AND KINB (BY SIMILARITY).
CC -I- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
CC
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DR EMBL; U09972; AAA18873.1; -
DR HSSP; P52934; 10MP.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; response_reg_1.
DR PRODOM; PD000039; Response_reg_1.
DR PROSITE; PS00110; RESPONSE_REGULATORY_1.
KW Sporulation; DNA-binding; Transcription regulation; Activator;
KW Repressor; Phosphorylation; Sensory transduction.
FT NON_TER 1

FT DOMAIN <1 59 RESPONSE REGULATORY.
FT DNA_BIND 132 >150 H-T-H MOTIF (POTENTIAL).
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16844 MW; 175977501F151D35 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 150;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 85 NLDA 88

RESULT 22
ISPF_LISTIN STANDARD; PRT; 157 AA.
ID ISPF_LISTIN
AC Q92P39;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
DE (MECPs) (MECDP-synthase).
GN ISPF OR L1N0268.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusnlok C., Amend A.,
BA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Denoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Eutlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tietze A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Converts 4-diphosphocytidyl-2C-methyl-D-erythritol 2-
phosphate into 2C-methyl-D-erythritol 2,4-cyclodiphosphate and
CMP. Also converts 4-diphosphocytidyl-2C-methyl-D-erythritol into
2C-methyl-D-erythritol 3,4-cyclodiphosphate and CMP (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-
methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
+ CMP.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step.
CC -1- SIMILARITY: BELONGS TO THE ISPF FAMILY.
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CC -----
DR EMBL: AL596164; GAC95501.1; -
DR Listlist; L1N00268; -
DR InterPro; IPR004423; ISPF.
DR Pfam; PF02542; Ygdb; 1.
DR TIGRfam; TIGR00151; ispf; 1.
DR PROSITE; PS01350; ISPF; 1.
KW Lyase; Isoprene biosynthesis; Complete proteome.
SQ SEQUENCE 157 AA; 17228 MW; 03E0B036A53E4C14 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
Db 94 NLDA 97

RESULT 23
ISPF_LISTMO STANDARD; PRT; 157 AA.
ID ISPF_LISTMO
AC Q8YAB4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
DE (MECPs) (MECDP-synthase).
GN ISPF OR LMO0236.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusnlok C., Amend A.,
BA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Denoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Eutlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkak G.,
RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tietze A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Converts 4-diphosphocytidyl-2C-methyl-D-erythritol 2-
phosphate into 2C-methyl-D-erythritol 2,4-cyclodiphosphate and
CMP. Also converts 4-diphosphocytidyl-2C-methyl-D-erythritol into
2C-methyl-D-erythritol 3,4-cyclodiphosphate and CMP (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-4-(cytidine 5'-diphospho)-2-C-
methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate
+ CMP.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fifth step.
CC -1- SIMILARITY: BELONGS TO THE ISPF FAMILY.
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CC -----
DR EMBL: AL591974; CAD00763.1; -
DR Listlist; LMO00236; -
DR InterPro; IPR004423; ISPF.
DR Pfam; PF02542; Ygdb; 1.
DR TIGRfam; TIGR00151; ispf; 1.
DR PROSITE; PS01350; ISPF; 1.
KW Lyase; Isoprene biosynthesis; Complete proteome.
SQ SEQUENCE 157 AA; 17029 MW; 7C1679D32553FDF8 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 24
NIFX_RHOCA
ID NIFX_RHOCA STANDARD; PRT; 159 AA.
AC P19078;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE NifX protein.
GN NIFX.
OS Rhodobacter capsulatus (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89313674; PubMed=2747620;
RA Moreno-Vivian C., Schmehl M., Masepohl B., Arnold W., Klipp W.;
RT "DNA sequence and genetic analysis of the Rhodobacter capsulatus
nifH gene region: homology between NifX and NifB suggests
involvement of NifX in processing of the iron-molybdenum cofactor.";
RT Mol. Gen. Genet. 216:353-363(1989).
RL -1- FUNCTION: MAY PLAY A ROLE IN THE PROCESSING OF THE IRON-
MOLYBDENUM COFACTOR.
CC -1- SIMILARITY: TO NIFB.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17433; CAA35474.1; -
DR PIR; J00031; J00031.
DR InterPro; IPR003731; DUF153.
DR Pfam; PF02579; DUF153; 1.
KW Nitrogen fixation.
SQ SEQUENCE 159 AA; 17456 MW; 8470D344B6C71005 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
DB 31 NIDA 34

RESULT 25
FLAV_CLOSA
ID FLAV_CLOSA STANDARD; PRT; 160 AA.
AC P18855;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flavodoxin.
GN FLOX.
OS Clostridium saccharobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=169679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91123180; PubMed=1991710;
RA Santangelo J.D., Jones D.T., Woods D.R.;
RT "Metronidazole activation and isolation of Clostridium acetobutylicum
electron transport genes.";
RT J. Bacteriol. 173:1088-1095(1991).
RL -1- FUNCTION: LOW-POTENTIAL ELECTRON DONOR TO A NUMBER OF REDOX
ENZYMES.
CC -----

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CC -1- COFACTOR: FMN.
CC -1- SIMILARITY: BELONGS TO THE FLAVODOXIN FAMILY.
CC -1- CAUTION: Was originally thought to originate from
CC C.acetobutylicum.
CC -----
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CC -----
DR EMBL; M36770; AAA23238.1; -
DR PIR; A38177; A38177.
DR InterPro; IPR001226; Flavodoxin.
DR Pfam; PF00258; Flavodoxin; 1.
DR PROSITE; PS00201; FLAVODOXIN; 1.
KW Electron transport; Flavoprotein; FMN.
SQ SEQUENCE 160 AA; 17763 MW; 6153F8A1F0BCD9D CRC64;

Query Match 100.0%; Score 20; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
DB 37 NIDA 40

RESULT 26
PHEA_SYNY1
ID PHEA_SYNY1 STANDARD; PRT; 164 AA.
AC P20778;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin alpha chain.
GN CPEA OR CPEA.
OS Synechocystis sp. (strain PCC 6701).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1144;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90170840; PubMed=2106507;
RA Anderson L.K., Grossman A.R.;
RT "Structure and light-regulated expression of phycoerythrin genes in
RT wild-type and phycoerythrin assembly mutants of Synechocystis sp.
RT strain PCC 6701."
RL J. Bacteriol. 172:1297-1305(1990).
RL -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Periphery of the rods of the phycoerythrin.
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
CC -----
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CC -----
DR EMBL; M36812; AAA27280.1; -
DR PIR; B35127; B35127.
DR HSPD; O36005; 1B8D.
DR InterPro; IPR001659; Phycoerythrin.
DR Pfam; PF00502; Phycoerythrin; 1.
DR PROSITE; PS00340; Phycoerythrin; 1.
KW Phycoerythrin; Electron transport; Photosynthesis; Bile pigment.
FT BINDING 82 82 PHYCOERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.

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SEQ SEQUENCE 164 AA: 17653 MW: 35CFB8503272E38F CRC64:

Query Match 100.0%; Score 20; DB 1; Length 164;

Best Local Similarity 100.0%; Pred. NO. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 47 NLDA 50

RESULT 27

NUE2_RHIME

ID NUE2_RHIME STANDARD; PRT; 168 AA.

AC P56910;

DT 30-MAY-2000 (Rel. 39, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE NADH dehydrogenase I chain E 2 (EC 1.6.5.3) (NADH-ubiquinone

oxidoreductase chain E 2).

GN NUOE2 OR RA0830 OR SMA1526.

OS Rhizobium melioli (Sinorhizobium melioli).

OC Plasmid pSyma (megaplasmid 1).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Sinorhizobium.

NCBI_TaxID=382;

[1]

SEQUENCE FROM N.A.

RC STRAIN=41;

RA Putnoky P., Jady B., Chellapilla K.P., Barta F., Kiss E.;

RT "Rhizobium melioli carries two sets of nuo genes."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.

RC STRAIN=1021;

RA MEDLINE=21396509; PubMed=11481432;

RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

RA Gurjal M., Hong A., Hultzer L., Hyman R.W., Kahn D., Kahn M.L.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RT "Nucleotide sequence and predicted functions of the entire

Sinorhizobium melioli pSyma megaplasmid."

RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).

CC -1-CATALYTIC ACTIVITY: NADH + ubiquinone -> NAD(+) + ubiquinol.

CC -1-CORCTOR: BINDS A 2FE-2S CLUSTER (POTENTIAL).

CC -1-SIMILARITY: BELONGS TO THE COMPLEX I 24 kDa SUBUNIT FAMILY.

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CC -----

CC EMBL: AJ245399; CAB51633.1; -

DR EMBL: AE007270; AAK65488.1; -

DR InterPro: IPR002023; Cmplx1_24kDa.

DR Pfam: PF01257; Cmplx1_24kD.1.

DR ProDom: PD003859; Cmplx1_24kDa: 1.

DR PROSITE: PS01059; Cmplx1_24k: 1.

KM Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; Plasmid;

KW Complete proteome.

FT METAL 77 IRON-SULFUR (2FE-2S) (POTENTIAL);

FT METAL 82 IRON-SULFUR (2FE-2S) (POTENTIAL);

FT METAL 118 IRON-SULFUR (2FE-2S) (POTENTIAL);

FT METAL 122 IRON-SULFUR (2FE-2S) (POTENTIAL);

FT CONFLICT 96 T->K (IN REF.1).

SEQ SEQUENCE 168 AA: 18375 MW: 165121F27B0C8948 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 168;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
||||
DB 137 NLDA 140

RESULT 28

YFIR_ECOLI

ID YFIR_ECOLI STANDARD; PRT; 172 AA.

AC P76597;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein yfir precursor.

GN YFIR OR B2603 OR Z3897 OR ECS3466.

OS Escherichia coli, and

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

NCBI_TaxID=562, 83334;

[1]

SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RA MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.A., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12."

RL Science 277:1453-1474(1997).

[2]

SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;

RA MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grobbeck E.J., Davis N.W., Llm A., Dinalanta E.T., Potomus K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blattner F.R.;

RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."

RL Nature 409:529-533(2001).

[3]

SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;

RA MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,

RA Kihara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohaemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12."

RL DNA Res. 8:11-22(2001).

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CC -----

CC EMBL: AE000346; AAC75652.1; -

DR EMBL: AE005490; AAG57714.1; -

DR EMBL: AP002562; BAB36889.1; -

DR EcoGene: EG14225; yfir.

KW Hypothetical protein; Signal; Complete proteome.

FT SIGNAL 1 POTENTIAL.

FT CHAIN 23 172 HYPOTHETICAL PROTEIN YFIR.

SEQ SEQUENCE 172 AA: 18978 MW: 2E2CC812E49F3AD5 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 172;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
DB 147 NLDA 150

RESULT 29

YMYL_CAEEL STANDARD; PRT; 176 AA.
ID YMYL_CAEEL
AC 011088;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C01C4.1 in chromosome X precursor.
GN C01C4.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
NCBI_TaxID=6239;

RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RP REVISIONS.
RA Waterston R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----

DR EMBL; U41025; AAA82349.2; -
DR WormPep; C01C4.1; CE29554.
KW Hypothetical protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 176
FT SEQUENCE 176 AA; 20081 MW; EF58809D2034267C CRC64;
SO

Query Match 100.0%; Score 20; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
DB 163 NLDA 166

RESULT 30

KADL_ANASP STANDARD; PRT; 184 AA.
ID KADL_ANASP
AC Q8RPJ8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase 1 (EC 2.7.4.3) (ATP-AMP transphosphorylase 1).
GN ADK1 OR ALKA196.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S.,
RA Kaneko T., Nakamura Y., Wolk C.P.,
RA Watanabe A., Irituchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakazaki N., Shampo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RU DNA Res. 8:205-213(2001).

CC -1- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC -----

DR EMBL; AF003595; BAB75895.1; -
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; adenylatekinase; 1.1
DR PRINTS; PRO0094; ADENYLTKINASE.
DR PRODOM; PD000657; Adenylate_kin; 1.1
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW transferase; Kinase; ATP-binding; Complete proteome.
FT NP_BIND 8 16
FT SEQUENCE 184 AA; 20442 MW; AOCEDB1170D93B69 CRC64;
SO

Query Match 100.0%; Score 20; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
DB 113 NLDA 116

RESULT 31

TBP_THECE STANDARD; PRT; 189 AA.
ID TBP_THECE
AC 056253;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TATA-box binding protein (TATA-box factor) (TATA sequence-binding
DE protein) (TBP) (Box A binding protein) (BAP).
GN TBP.

OS Thermococcus celer.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
NCBI_TaxID=2264;
[1]

RP SEQUENCE FROM N.A.
RX STRAIN=DSM 2476;
RX MEDLINE=94240101; PubMed=8183889;
RA Marsh T.L., Reich C.I., Whitelock R.B., Olsen G.J.;
RT "Transcription factor IID in the Archaea: sequences in the
RT Thermococcus celer genome would encode a product closely related to
RT the TATA-binding protein of eukaryotes.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4180-4184(1994).
CC -1- FUNCTION: GENERAL FACTOR THAT PLAYS A ROLE IN THE ACTIVATION OF
CC ARCHAEAL GENES TRANSCRIBED BY RNA POLYMERASE. BINDS SPECIFICALLY
CC TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO THE POSITION
CC OF TRANSCRIPTION INITIATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TBP FAMILY.

CC -----
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CC  -----
DR  EMBL: U04932; AAA73412.1; -.
DR  HSSP: Q57050; 1PCZ.
DR  InterPro: IPR000814; TFIID.
DR  Pfam: PF00352; TBP; 2.
DR  PRINTS: PR00686; TIFACTORIID.
DR  PROSITE: PS00351; TFIID; 2.
KW  Transcription regulation; DNA-binding; Repeat.
FT  REPEAT      8      84
FT  REPEAT      99     175
SQ  SEQUENCE    189 AA; 21348 MW; 1FE1509E645E7980 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 189;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 NLDA 4
DB  113 NLDA 116

RESULT 32
TBP_PYRKO
ID  TBP_PYRKO      STANDARD; PRT; 190 AA.
AC  052366;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  TATA-box binding protein (TATA-box factor) (TATA sequence-binding
DE  protein) (TBP) (Box A binding protein) (BAP).
GN  TBP.
OS  Pyrococcus kodakarensis.
OC  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC  Thermococcus.
OX  NCBI_TaxID=69014;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=KOD1;
RX  MEDLINE=96105215; PubMed=8529878;
RA  Rashid N., Morikawa M., Imanaka T.;
RT  "An abnormally acidic TATA-binding protein from a hyperthermophilic
RT  archaeon".
RL  Gene 166:139-143(1995).
CC  -I- FUNCTION: GENERAL FACTOR THAT PLAYS A ROLE IN THE ACTIVATION OF
CC  ARCHAICAL GENES TRANSCRIBED BY RNA POLYMERASE. BINDS SPECIFICALLY
CC  TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO THE POSITION
CC  OF TRANSCRIPTION INITIATION.
CC  -I- SIMILARITY: BELONGS TO THE TBP FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: D50018; BAA08743.1; -.
DR  HSSP: Q57050; 1PCZ.
DR  InterPro: IPR000814; TFIID.
DR  Pfam: PF00352; TBP; 2.
DR  PRINTS: PR00686; TIFACTORIID.
DR  PROSITE: PS00351; TFIID; 2.
KW  Transcription regulation; DNA-binding; Repeat.
FT  REPEAT      11     87
FT  REPEAT      102    178
SQ  SEQUENCE    190 AA; 21494 MW; 503115E5B077077D CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 190;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY  1 NLDA 4
DB  116 NLDA 119

RESULT 33
SPOA_BACPU
ID  SPOA_BACPU      STANDARD; PRT; 191 AA.
AC  P52933;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Stage 0 sporulation protein A (Fragment).
GN  SPOA.
OS  Bacillus pumilus (Bacillus mesentericus).
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX  NCBI_TaxID=1408;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PB4;
RX  MEDLINE=95191392; PubMed=785226;
RA  Brown D.P., Gancova-Raeva L., Green B.D., Wilkinson S.R., Young M.,
RA  Youngman P.;
RT  "Characterization of spoA homologues in diverse Bacillus and
RT  Clostridium species identifies a probable DNA-binding domain.";
RL  Mol. Microbiol. 14:411-426(1994).
CC  -I- FUNCTION: MAY PLAY THE CENTRAL REGULATORY ROLE IN SPOULATION. IT
CC  MAY BE AN ELEMENT OF THE EFFECTOR PATHWAY RESPONSIBLE FOR THE
CC  ACTIVATION OF SPOULATION GENES IN RESPONSE TO NUTRITIONAL STRESS.
CC  SPOA MAY ACT IN CONCERT WITH SPOOH (A SIGMA FACTOR) TO CONTROL
CC  THE EXPRESSION OF SOME GENES THAT ARE CRITICAL TO THE SPOULATION
CC  PROCESS. REPRESSOR OF ABRB, ACTIVATOR OF THE SPOIIA OPERON. BINDS
CC  THE DNA SEQUENCE 5'-TGCGAA-3' (OA BOX) (BY SIMILARITY).
CC  -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC  -I- PTM: PHOSPHORYLATED BY KINA AND KINB (BY SIMILARITY).
CC  -I- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
CC  -----
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CC  -----
DR  EMBL: U09975; AAA18876.1; -.
DR  HSSP: P52934; 1OMP.
DR  InterPro: IPR001789; Response_reg.
DR  Pfam: PF00072; Response_reg; 1.
DR  ProDom: PD000039; Response_reg; 1.
DR  PROSITE: PS50110; RESPONSE_REGULATORY; 1.
KW  Sporulation; DNA-binding; Transcription regulation; Activator;
KW  Repressor; Phosphorylation; Sensory transduction.
FT  NON_TER      1
FT  DOMAIN       <1     60
FT  DNA_BIND     136    155
FT  NON_TER      191    191
FT  H-T-H MOTIF (POTENTIAL).
SQ  SEQUENCE    191 AA; 21288 MW; D211F2C695F56B44 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 191;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 NLDA 4
DB  89 NLDA 92

RESULT 34
TXLA_SYNP7
ID  TXLA_SYNP7      STANDARD; PRT; 191 AA.
AC  P35088;

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DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Thiol:disulfide Interchange protein txa1.
GN TXLA.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxId=1140;
RN [1]
RP SEQUENCE FROM N.A.
RA Collier J.L., Grossman A.R.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REQUIRED FOR DISULFIDE BOND FORMATION IN SOME PROTEINS.
CC ACTS BY TRANSFERRING ITS DISULFIDE BOND TO OTHER PROTEINS AND IS
CC REDUCED IN THE PROCESS.
CC -1- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC -----
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CC -----
DR EMBL: U05044; AAA89104.1; -.
DR HSSP: P20857; 1THX.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF000085; thioRed; 1.
DR PROSITE: PS00194; THIOREDOXIN; 1.
KW Redox-active center; Transmembrane.
FT TRANSMEM 14 30 POTENTIAL.
FT DISULFID 69 72 REDOX-ACTIVE (POTENTIAL).
SQ SEQUENCE 191 AA; 20661 MW; 8C88B397AD40F640 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 191;
Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
Db 142 NIDA 145

RESULT 35
INDL HUMAN
ID INDL HUMAN STANDARD; PRT; 195 AA.
AC P37290;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interferon delta-1 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94193794; PubMed=7511610;
RA Whaley A.E., Meka C.S.R., Reddy C.S., Harbison L.A., Hunt J.S.,
RA Imakawa K.;
DE "Identification and cellular localization of unique interferon mRNA
DE from human placenta.";
RL J. Biol. Chem. 269:10864-10868(1994).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
CC -----
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CC -----
DR EMBL: L25664; AAA36123.1; -.
DR PIR: A53746; A53746.
DR HSSP: P01563; 2HIE.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR Prodom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; Irbad; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 195 INTERFERON DELTA-1.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 195 AA; 21898 MW; E81CF9E29E29165 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 195;
Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
Db 118 NIDA 121

RESULT 36
YDB6 YEAST
ID YDB6 YEAST STANDARD; PRT; 197 AA.
AC Q12055;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 22.7 kDa protein in CDC36-NRP1 intergenic region.
GN YDL166C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Pohl T.M.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE UPF0101 FAMILY.
CC -----
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CC -----
DR EMBL: 267750; CA91580.1; -.
DR EMBL: Z74214; CA98740.1; -.
DR SGD: S0002325; YDL166C.
KW Hypothetical protein; Arp-binding.
FT NP BIND 14 21 ARP (POTENTIAL).
SQ SEQUENCE 197 AA; 22723 MW; 836425BBD7E2633C CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 197;
Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
Db 124 NIDA 127

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RESULT 37
GDIR_YEAST      STANDARD;      PRT;      202 AA.
ID   GDIR_YEAST
AC   012434;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Rho GDP-dissociation inhibitor (Rho GDI).
GN   RDI1 OR YDL135C OR D2175.
OC   Saccharomyces cerevisiae (Baker's yeast).
OS   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxId=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94327511; PubMed=8051050;
RA   Masuda T., Tanaka K., Nonaka H., Yamochi W., Maeda A., Takai Y.;
RT   "Molecular cloning and characterization of yeast rho GDP dissociation
RL   inhibitor."
RL   J. Biol. Chem. 269:19713-19718(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=5286c / FY1679;
RX   MEDLINE=97127826; PubMed=8972577;
RA   Moell S., Haneman V., Saluz H.P.;
RT   "Analysis of a 26,756 bp segment from the left arm of yeast
RL   chromosome IV."
RL   Yeast 12:1549-1554(1996).
CC   -1- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF THE RHO
CC   PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE
CC   SUBSEQUENT BINDING OF GTP TO THEM.
CC   -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -1- SIMILARITY: BELONGS TO THE RHO GDI FAMILY.
CC   -----
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CC   -----
DR   EMBL; D31630; BAA06499.1; -
DR   EMBL; X96876; CAA65624.1; -
DR   EMBL; Z74183; CAA98708.1; -
DR   HSSP; P52566; IDS6.
DR   SGD; S0002294; RDI1.
DR   InterPro; IPR000406; Rho_GDI.
DR   Pfam; PF02115; Rho_GDI; 1.
KW   GTPase activation.
SQ   SEQUENCE 202 AA; 23138 MW; 300FF974383B496F CRC64;
Query Match      100.0%; Score 20; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLDA 4
DB 33 NLDA 36

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OX   NCBI_TaxId=2371;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=945c;
RX   MEDLINE=20365717; PubMed=10910347;
RA   Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA   Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA   Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
RA   Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA   Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA   Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA   Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferio J.A.,
RA   Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA   Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA   Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitaajima J.P.,
RA   Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA   Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA   Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA   Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA   Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA   Moon D.H., Nagai M.A., Nascimento A.L.T.O., Neto L.E.S.,
RA   Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA   de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA   Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
RA   Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA   de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA   da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA   da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA   de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA   Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA   Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT   "The genome sequence of the plant pathogen Xylella fastidiosa."
RL   Nature 406:151-159(2000).
CC   -1- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE 3'-HYDROXYL GROUP
CC   OF DEPHOSPHOCOENZYME A TO FORM COENZYME A (BY SIMILARITY).
CC   -1- CATALYTIC ACTIVITY: ATP + dephospho-CoA = ADP + CoA.
CC   -1- PATHWAY: Coenzyme A (CoA) biosynthesis; fifth (last) step.
CC   -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -1- SIMILARITY: BELONGS TO THE COAE FAMILY.
CC   -----
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CC   -----
DR   EMBL; AE004060; AAF85333.1; ALT_INIT.
DR   InterPro; IPR001977; Depp-CoAkinase.
DR   Pfam; PF01121; Coae; 1.
DR   ProDom; PD003329; Depp-CoAkinase; 1.
DR   TIGRFAMs; TIGR00152; UPP0038; 1.
DR   PROSITE; PS01294; COAE; 1.
KW   Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
KW   Complete proteome.
FT   NP_BIND 10
SQ   SEQUENCE 207 AA; 22224 MW; FB6234199F314CD8 CRC64;
Query Match      100.0%; Score 20; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLDA 4
DB 191 NLDA 194

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RESULT 39
VS10_ROTBS      STANDARD;      PRT;      209 AA.
ID   VS10_ROTBS
AC   P34718;
DT   01-FEB-1994 (Rel. 28, Created)

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DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Minor outer capsid protein (NS26).
 CC S10.
 OS Bovine rotavirus (group C / strain Shintoku).
 CC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
 CC NCBI_TaxID=33723;
 RX MEDLINE=93275758; PubMed=8389040;
 RA Jiang B., Tsunemitsu H., Gentsch J.R., Saif L.J., Glass R.I.;
 RT "Nucleotide sequences of genes 6 and 10 of a bovine group C
 rotavirus.";
 RL Nucleic Acids Res. 21:2250-2250(1993).
 CC -----
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 CC -----
 DR EMBL; L12391; NOT_ANNOTATED_CDS.
 DR InterPro; IPR002512; Rota_NS26.
 DR Pfam; PF01525; Rota_NS26; 1.
 KW Coat protein.
 SQ SEQUENCE 209 AA; 23438 MW; 820AC9B3C9DA1956 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 209;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
 ||||
 Db 7 NIDA 10

RESULT 40
 SP0A_BACCI STANDARD; PRT; 210 AA.
 ID SP0A_BACCI
 AC P52931;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stage 0 sporulation protein A (Fragment).
 GN SP0A.
 OS Bacillus circulans.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC NCBI_TaxID=1397;
 RX NCBI_TaxID=1397;
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 4513;
 RX MEDLINE=95191392; PubMed=7885226;
 RA Brown D.P., Ganova-Raeva L., Green B.D., Wilkinson S.R., Young M.,
 RA Youngman P.;
 RT "Characterization of sp0A homologues in diverse Bacillus and
 RT Clostridium species identifies a probable DNA-binding domain.";
 RL Mol. Microbiol. 14:411-426(1994).
 CC -----
 CC -1- FUNCTION: MAY PLAY THE CENTRAL REGULATORY ROLE IN SPOULATION. IT
 CC MAY BE AN ELEMENT OF THE RECEPTOR PATHWAY RESPONSIBLE FOR THE
 CC ACTIVATION OF SPOULATION GENES IN RESPONSE TO NUTRITIONAL STRESS.
 CC SP0A MAY ACT IN CONCERT WITH SPOOH (A SIGMA FACTOR) TO CONTROL
 CC THE EXPRESSION OF SOME GENES THAT ARE CRITICAL TO THE SPOULATION
 CC PROCESS. REPRESSOR OF ABBR, ACTIVATOR OF THE SPOIIA OPERON. BINDS
 CC THE DNA SEQUENCE 5'-TGCGAA-3' (OA BOX) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- PTM: PHOSPHORYLATED BY KINA AND KINB (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U09973; AAA1874.1; -;
 DR HSP; P52934; 10MP.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF00072; response_reg; 1.
 DR Prodom; PD000039; Response_reg; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW Sporulation; DNA-binding; Transcription regulation; Activator;
 KW Repressor; Phosphorylation; Sensory transduction.
 FT DOMAIN 1 122
 FT DNA_BIND 192 >210
 FT MOD_RES 56 56
 FT NON_TER 210 210
 SQ SEQUENCE 210 AA; 23688 MW; D75E1CE5FB32456 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
 ||||
 Db 145 NIDA 148

RESULT 41
 VS10_ROTPO STANDARD; PRT; 210 AA.
 ID VS10_ROTPO
 AC P36358;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Minor outer capsid protein (NS26).
 GN S10.
 OS Porcine rotavirus (group C / strain Cowden).
 CC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
 CC NCBI_TaxID=10916;
 RX NCBI_TaxID=10916;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93277387; PubMed=8389118;
 RA Brement M., Chabanne-Vautherot D., Cohen J.;
 RT "Sequence analysis of three non structural proteins of a porcine
 RT group C (Cowden strain) rotavirus.";
 RL Arch. Virol. 130:85-92(1993).
 CC -----
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 CC -----
 DR EMBL; X65938; CAA46741.1; -;
 DR PIR; B48357; B48357.
 DR PIR; S25544; S25544.
 DR InterPro; IPR002512; Rota_NS26.
 DR Pfam; PF01525; Rota_NS26; 1.
 KW Coat protein.
 SQ SEQUENCE 210 AA; 23393 MW; 4A3C9910803B0943 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
 ||||
 Db 7 NIDA 10

```

RESULT 42
SODF_ACIAM          STANDARD:      PRT:      211 AA.
ID  SODF_ACIAM
AC  09P9L3;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DE  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Superoxide dismutase [Fe] (EC 1.15.1.1).
GN  SOD.
OS  Acidianus ambivalens (Desulfurolobus ambivalens).
OC  Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC  Acidianus.
OX  NCBI_TaxID=2283;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  MEDLINE=21026956; Pubmed=11154067;
RT  "The hyper-thermostable Fe-superoxide dismutase from the Archaeon
RT  Acidianus ambivalens: characterization, recombinant expression,
RT  crystallization and effects of metal exchange.";
RT  Biol.Chem. 381:1089-1101(2000).
CC  -1- FUNCTION: Destroys radicals which are normally produced within the
CC  cells and which are toxic to biological systems (By similarity).
CC  -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC  -1- COFACTOR: Iron (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC  FAMILY.
-----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
CC  EMBL: AF236110; AAF36989.1; -.
CC  HSSP: P80857; 1SSS.
CC  InterPro: IPR001189; SODismutase.
CC  Pfam: PF00081; sode; 1.
CC  Pfam: PF02777; sode; 1.
CC  DR  ProDom: PD000475; SODismutase; 1.
CC  DR  PROSITE: PS00088; SOD_MN; FALSE_NEG.
CC  KM  Oxidoreductase: Iron.
CC  FT  METAL 34 34 IRON (BY SIMILARITY).
CC  FT  METAL 82 82 IRON (BY SIMILARITY).
CC  FT  METAL 171 171 IRON (BY SIMILARITY).
CC  FT  METAL 175 175 IRON (BY SIMILARITY).
CC  SQ  SEQUENCE 211 AA; 24342 MW; 5A88FEE400F77065 CRC64;

Query Match          100.0%; Score 20; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 NIDA 4
    ||||
DB  18 NIDA 21

RESULT 43
IL6_CERTO
ID  IL6_CERTO          STANDARD:      PRT:      212 AA.
AC  P46550;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Interleukin-6 precursor (IL-6).
GN  IL6.
OS  Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC  Cercopithecinae; Cercopithecus.

```

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OX  NCBI_TaxID=9531;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=FUJ;
RX  MEDLINE=96003435; Pubmed=7561102;
RA  Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT  "Comparative sequence analysis of cytokine genes from human and
RT  nonhuman primates.";
RL  J. Immunol. 155:3946-3954(1995).
CC  -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC  FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC  OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC  PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC  HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
-----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
CC  EMBL: L26032; AAA99972.1; -.
CC  HSSP: P05231; 1ALT.
CC  InterPro: IPR003573; IL6_MGF_GCSF.
CC  InterPro: IPR003574; Interleukin_6.
CC  Pfam: PF00489; IL6; 1.
CC  DR  PRINTS: PR00433; IL6GCSFMGF.
CC  DR  ProDom: PD004356; Interleukin_6; 1.
CC  DR  SMART: SM00126; IL6; 1.
CC  DR  PROSITE: PS00254; INTERLEUKIN_6; 1.
CC  KW  Cytokine; Glycoprotein; Growth factor; Signal.
CC  FT  SIGNAL 1 29 BY SIMILARITY.
CC  FT  CHAIN 30 212 INTERLEUKIN-6.
CC  FT  DISULFID 72 78 POTENTIAL.
CC  FT  DISULFID 101 111 POTENTIAL.
CC  FT  CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC  FT  CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC  SQ  SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match          100.0%; Score 20; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 NIDA 4
    ||||
DB  160 NIDA 163

RESULT 44
IL6_HUMAN
ID  IL6_HUMAN          STANDARD:      PRT:      212 AA.
AC  P05231;
DT  13-AUG-1987 (Rel. 05, Created)
DT  13-AUG-1987 (Rel. 05, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2)
DE  (Interferon beta-2) (Hypridoma growth factor).
GN  IL6 OR IFNB2.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA  MEDLINE=87065033; Pubmed=3491322;
RA  Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
RA  Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
RA  Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
RT  "Complementary DNA for a novel human interleukin (BSF-2) that induces

```


RT B lymphocytes to produce immunoglobulin.";
 RL Nature 324:73-76(1986).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86082664; PubMed=3500852;
 RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
 Nakai S., Kishimoto T.;
 RT "Structure and expression of human B cell stimulatory factor-2
 (BSF-2/IL-6) gene.";
 RL EMBO J. 6:2935-2945(1987).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87067433; PubMed=3538015;
 RA May L.T., Helfgott D.C., Sehgal P.B.;
 RT "Anti-beta-interferon antibodies inhibit the increased expression of
 HTA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 RT structural studies of the beta 2 interferon involved.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87053818; PubMed=3023045;
 RA Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
 RT "Structure and expression of cDNA and genes for human
 RT interferon-beta-2, a distinct species inducible by growth-stimulatory
 RT cytokines.";
 RL EMBO J. 5:2529-2537(1986).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88088768; PubMed=3320204;
 RA Braehenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 Aarden L.A.;
 RT "Molecular cloning and expression of hybridoma growth factor in
 RT Escherichia coli.";
 RL J. Immunol. 139:4116-4121(1987).
 RN [16]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89391958; PubMed=2789513;
 RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
 RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [17]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87004683; PubMed=3758081;
 RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [18]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89193317; PubMed=3266463;
 RA Wong G., Witek-Gianotti J., Hewick R., Clark S., Ogawa M.;
 RT "Interleukin 6: identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [19]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93178270; PubMed=1291290;
 RA Chen Q.Y.;
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [110]
 RP SEQUENCE FROM N.A., AND VARIANTS SER-32 AND VAL-162.
 RA Rieder M.J., Carington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,
 RA Nickerson D.A.;
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [111]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;

RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [112]
 RP SEQUENCE OF 30-63.
 RX MEDLINE=88154445; PubMed=3279116;
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 Billiau A.;
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [113]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE BOND.
 RX MEDLINE=95154344; PubMed=7851440;
 RA Breton J., la Fluta A., Bertolero F., Orsini G., Valasina B.,
 RA Zillicotto R., de Filipis V., Polymerio de lauro P., Fontana A.;
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [114]
 RP DISULFIDE BONDS.
 RX MEDLINE=89286115; PubMed=2472117;
 RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [115]
 RP MUTAGENESIS.
 RX MEDLINE=91243808; PubMed=2037043;
 RA Luetticken C., Krueitgen A., Moeller C., Heinrich P.C., Rose-John S.;
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [116]
 RP STRUCTURE BY NMR.
 RX MEDLINE=96134845; PubMed=8555185;
 RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [117]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97303053; PubMed=9159484;
 RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RT "Solution structure of recombinant human interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [118]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97224126; PubMed=9118960;
 RA Somers W., Stahl M., Seehra J.S.;
 RT "1.9-A crystal structure of interleukin 6: implications for a novel
 RT mode of receptor dimerization and signaling.";
 RL EMBO J. 16:989-997(1997).
 CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -I- SUBCELLULAR LOCATION: Secreted;
 CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -I- DATABASE: NAME-Rad Systems' cytokine mini-reviews: IL6;
 CC WWW="http://www.rndsystems.com/ssp/g-sitebuilder.asp?bodyid=208".
 CC -----
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CC -----
DR EMBL: X04430; CAA28026.1; -
DR EMBL: M14584; AAA52728.1; -
DR EMBL: X04602; CAA28268.1; -
DR EMBL: X00081; CAA68278.1; -
DR EMBL: M18403; AAA52729.1; -
DR EMBL: M29150; CAA27990.1; -
DR EMBL: X04402; CAA27991.1; -
DR EMBL: M54894; AAC41704.1; -
DR EMBL: S56892; AAD13886.1; -
DR EMBL: AF372214; AAK48987.1; -
DR EMBL: BC015511; AAH15511.1; -
DR EMBL: A09363; CAA00839.1; -
DR PIR: A32648; IVHUB2.
DR PIR: A25921; A25921.
DR PDB: 1IL6; 04-FEB-98.
DR PDB: 2IL6; 04-FEB-98.
DR PDB: 1ALU; 03-JUN-98.
DR Genew; HGNC:6018; IL6.
DR MIM: 147620; -.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Glycoprotein; Growth factor; Signal; Polymorphism;
KM 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .).
FT

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Query Match          100.0%; Score 20; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NLDA 4
Db 160 NLDA 163

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RESULT 45
IL6_MACFA          STANDARD;          PRT;          212 AA.
ID IL6_MACFA          P79341;
DR 15-JUL-1998 (Rel. 36, Created)
DR 15-JUL-1998 (Rel. 36, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatum M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOID AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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```

CC -----
DR EMBL: AB000554; BAA19148.1; -
DR HSSP: P05231; IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Glycoprotein; Growth factor; Signal.
KM 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23654 MW; CF81J3FCBF0B0389 CRC64;

```

```

Query Match          100.0%; Score 20; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NLDA 4
Db 160 NLDA 163

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Search completed: February 6, 2003, 11:16:51
Job time : 7.33333 secs

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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 21.3333 Seconds
(without alignments)
38.634 Million cell updates/sec

Title: PAT943-6
Perfect score: 20
Sequence: 1 nlda 4

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 2343

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvitus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	26	5	Q9BM03 dugesia tig
2	20	100.0	33	5	Q9GTC2 dugesia tig
3	20	100.0	33	5	Q9GTC2 plasmidium
4	20	100.0	33	5	Q9GTC2 eimeria ten
5	20	100.0	33	5	Q9GTC2 sarcocystis
6	20	100.0	33	5	Q9GTC2 babesia bov
7	20	100.0	33	5	Q9GTC2 cryptospori
8	20	100.0	41	6	Q9N194 macaca muli
9	20	100.0	41	6	Q9N193 gorilla gor
10	20	100.0	41	6	Q9N192 pan troglod
11	20	100.0	42	2	Q53299 hylobates i
12	20	100.0	42	15	Q9G582 human immu
13	20	100.0	50	5	Q8TF64 ceratilis c
14	20	100.0	50	5	Q8TF64 ceratilis c
15	20	100.0	51	16	Q8RAW6 thelmonaer
16	20	100.0	54	16	Q992Y5 streptococ

17	20	100.0	57	12	Q91TH0	Q91TH0 tupia herp
18	20	100.0	66	3	Q96X11	Q96X11 phaeosphaer
19	20	100.0	68	5	Q9TXV3	Q9TXV3 caenorhabdi
20	20	100.0	69	12	Q8VA17	Q8VA17 white spot
21	20	100.0	71	2	Q93PT2	Q93PT2 lactococcus
22	20	100.0	72	16	Q99TW2	Q99TW2 staphylococ
23	20	100.0	73	4	Q95641	Q95641 homo sapien
24	20	100.0	73	16	Q8X2G0	Q8X2G0 escherichia
25	20	100.0	75	16	Q9PND7	Q9PND7 campylobact
26	20	100.0	75	16	Q8XVB9	Q8XVB9 ralsstonia s
27	20	100.0	80	5	Q8TF40	Q8TF40 apis mellif
28	20	100.0	83	10	Q9AXX2	Q9AXX2 brassica na
29	20	100.0	85	10	Q9AXX0	Q9AXX0 brassica ca
30	20	100.0	86	16	Q8X6S5	Q8X6S5 escherichia
31	20	100.0	86	5	Q8TF41	Q8TF41 manduca sex
32	20	100.0	88	2	Q9XSH7	Q9XSH7 helicobacte
33	20	100.0	89	2	Q9AKH6	Q9AKH6 rickettsia
34	20	100.0	89	16	Q92J16	Q92J16 rickettsia
35	20	100.0	91	4	Q9H4V4	Q9H4V4 homo sapien
36	20	100.0	91	16	Q07938	Q07938 bacillus su
37	20	100.0	91	16	Q97KS3	Q97KS3 clostridium
38	20	100.0	92	2	Q9N5Z2	Q9N5Z2 escherichia
39	20	100.0	92	12	Q99H35	Q99H35 helicoverpa
40	20	100.0	93	16	Q8ZAU6	Q8ZAU6 yersinia pe
41	20	100.0	95	16	Q9K0G0	Q9K0G0 neisseria m
42	20	100.0	96	8	Q79692	Q79692 stigmatura
43	20	100.0	97	5	Q9V9P1	Q9V9P1 dtrosophila
44	20	100.0	101	2	Q9R9X3	Q9R9X3 pseudomonas
45	20	100.0	102	8	Q20641	Q20641 anabas test

ALIGNMENTS

RESULT 1

ID	Q9BM03	PRELIMINARY;	PRT;	26 AA.
AC	Q9BM03;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	Mariner-like transposase (Fragment).			
OS	Dugesia tigrida (Planarian).			
OC	Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Sertata; Tricladida;			
CC	Paludicola; Dugesidae; Girardia.			
OK	NCBI_TaxID=6162;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TRANSPON-MARMI;			
RX	MEDLINE=20570504; PubMed=11121049;			
RA	Arkhipova I., Meselson M.;			
RT	"Transposable elements in sexual and ancient asexual taxa.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).			
DR	EMBL; AY014003; AAG59975.1; -			
FT	NON_TER	1	1	
FT	NON_TER	1	1	
SQ	SEQUENCE	26 AA;	2946 MW;	74D1AD8CAADA347 CRC64;

Query Match 100.0%; Score 20; DB 5; Length 26;
Best local similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
DB 15 NIDA 18

RESULT 2

ID	Q9GTC2	PRELIMINARY;	PRT;	33 AA.
AC	Q9GTC2;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			

```
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Myosin D (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21215633; PubMed=11318578;
RA Heintzelman M.B., Schwartzman J.D.;
RT "Myosin diversity in Apicomplexa.";
RL J. Parasitol. 87:429-432(2001).
DR EMBL; AF273845; AAG29107.1; -.
DR InterPro; IPR001609; myosin_head.
DR Prodom; PD000355; myosin_head; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 33 AA; 3638 MW; 2E0CFB42104F2290 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 33;
Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
DB 17 NIDA 20

RESULT 3
Q9GTA2 PRELIMINARY; PRT; 33 AA.
ID Q9GTA2;
AC Q9GTA2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Myosin E (Fragment).
OS Eimeria tenella.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
OC Eimeria.
OX NCBI_TaxID=5802;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21215633; PubMed=11318578;
RA Heintzelman M.B., Schwartzman J.D.;
RT "Myosin diversity in Apicomplexa.";
RL J. Parasitol. 87:429-432(2001).
DR EMBL; AF273855; AAG29117.1; -.
DR InterPro; IPR001609; myosin_head.
DR Prodom; PD000355; myosin_head; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 33 AA; 3638 MW; 2E0CFB42104F2290 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 33;
Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
DB 17 NIDA 20

RESULT 4
Q9GTA9 PRELIMINARY; PRT; 33 AA.
ID Q9GTA9;
AC Q9GTA9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Myosin B (Fragment).
OS Sarcocystis muris.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Sarcocystis.
OX NCBI_TaxID=5813;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21215633; PubMed=11318578;
RA Heintzelman M.B., Schwartzman J.D.;
RT "Myosin diversity in Apicomplexa.";
RL J. Parasitol. 87:429-432(2001).
DR EMBL; AF273858; AAG29120.1; -.
DR InterPro; IPR001609; myosin_head.
DR Prodom; PD000355; myosin_head; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 33 AA; 3638 MW; 2E0CFB42104F2290 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 33;
Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
DB 17 NIDA 20

RESULT 5
Q9GTA2 PRELIMINARY; PRT; 33 AA.
ID Q9GTA2;
AC Q9GTA2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Myosin D (Fragment).
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21215633; PubMed=11318578;
RA Heintzelman M.B., Schwartzman J.D.;
RT "Myosin diversity in Apicomplexa.";
RL J. Parasitol. 87:429-432(2001).
DR EMBL; AF273865; AAG29127.1; -.
DR InterPro; IPR001609; myosin_head.
DR Prodom; PD000355; myosin_head; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 33 AA; 3638 MW; 2E0CFB42104F2290 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 33;
Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIDA 4
DB 17 NIDA 20

RESULT 6
Q9GTA5 PRELIMINARY; PRT; 33 AA.
ID Q9GTA5;
AC Q9GTA5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Myosin D (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21215633; PubMed=11318578;
RA Heintzelman M.B., Schwartzman J.D.;
RT "Myosin diversity in Apicomplexa.";
RL J. Parasitol. 87:429-432(2001).
```

DR EMBL: AF273872; AAG29134.1; -.
 DR InterPro: IPR001609; myosin_head.
 DR Prodom: PD000355; myosin_head.1.

FT NON_TER 1 1
 FT NON_TER 33 33
 SQ SEQUENCE 33 AA; 3638 MW; 2E0CFB42104F2290 CRC64;

Query Match 100.0%; Score 20; DB 5; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 17 NLDA 20

RESULT 7
 O9N194 PRELIMINARY; PRT; 41 AA.

AC 09N194: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Soluble guanylyl cyclase subunit beta 2 (Fragment).
 GN GUCY1B2.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20241821; PubMed=10777682;

RA Behrends S., Vohse K.;
 RT "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-Specific Frameshift and Is Expressed in Gastric Carcinoma.";
 RL Biochem. Biophys. Res. Commun. 271:64-69(2000).

DR EMBL: AF218384; AAF66106.1; -.
 FT NON_TER 1 1
 FT NON_TER 41 41
 SQ SEQUENCE 41 AA; 4948 MW; 31ACA70C4358DC1 CRC64;

Query Match 100.0%; Score 20; DB 6; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 28 NLDA 31

RESULT 8
 O9N193 PRELIMINARY; PRT; 41 AA.

AC 09N193: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Soluble guanylyl cyclase subunit beta 2 (Fragment).
 GN GUCY1B2.

OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
 OX NCBI_TaxID=9593;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20241821; PubMed=10777682;

RA Behrends S., Vohse K.;
 RT "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-Specific Frameshift and Is Expressed in Gastric Carcinoma.";
 RL Biochem. Biophys. Res. Commun. 271:64-69(2000).
 DR EMBL: AF218385; AAF66107.1; -.
 FT NON_TER 1 1

FT NON_TER 41 41
 SQ SEQUENCE 41 AA; 4888 MW; 31ACA718FCTE6DC1 CRC64;

Query Match 100.0%; Score 20; DB 6; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 28 NLDA 31

RESULT 9
 O9N192 PRELIMINARY; PRT; 41 AA.

AC 09N192: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Soluble guanylyl cyclase subunit beta 2 (Fragment).
 GN GUCY1B2.

OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_TaxID=9598;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20241821; PubMed=10777682;
 RA Behrends S., Vohse K.;
 RT "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-Specific Frameshift and Is Expressed in Gastric Carcinoma.";
 RL Biochem. Biophys. Res. Commun. 271:64-69(2000).

DR EMBL: AF218386; AAF66108.1; -.
 FT NON_TER 1 1
 FT NON_TER 41 41
 SQ SEQUENCE 41 AA; 4888 MW; 31ACA718FCTE6DC1 CRC64;

Query Match 100.0%; Score 20; DB 6; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 Db 28 NLDA 31

RESULT 10
 O9N191 PRELIMINARY; PRT; 41 AA.

AC 09N191: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Soluble guanylyl cyclase subunit beta 2 (Fragment).
 GN GUCY1B2.

OS Hylobates lar (Common gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9580;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20241821; PubMed=10777682;

RA Behrends S., Vohse K.;
 RT "The beta(2) Subunit of Soluble Guanylyl Cyclase Contains a Human-Specific Frameshift and Is Expressed in Gastric Carcinoma.";
 RL Biochem. Biophys. Res. Commun. 271:64-69(2000).

DR EMBL: AF218387; AAF66109.1; -.
 FT NON_TER 1 1
 FT NON_TER 41 41
 SQ SEQUENCE 41 AA; 4847 MW; 0B9F972BFC7E6DC1 CRC64;

Query Match 100.0%; Score 20; DB 6; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
Db 28 NLDA 31

RESULT 11

O53299 PRELIMINARY; PRT; 42 AA.
AC O53299;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE AphA1 protein (Fragment).
GN APHA1.
OS Escherichia coli.
OC Plasmid pIP1516.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93159149; Pubmed=8381641.
RA Menard R., Molinas C., Arthur M., Duval J., Courvalin P., Leclercq R.;
RT "Overproduction of 3'-aminoglycoside phosphotransferase type I confers
resistance to tobramycin in Escherichia coli.";
RL Antimicrob. Agents Chemother. 37:78-83(1993).
DR EMBL: S54065; AAD13871.1; -.
DR InterPro: IPR002575; APH.
DR Pfam: PF01636; APH. 1.
KW Plasmid.
KW NON_TER
SQ SEQUENCE 42 AA; 4831 MW; D6894835CE24D87 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
Db 18 NLDA 21

RESULT 12

O90582 PRELIMINARY; PRT; 42 AA.
AC O90582;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Envelope glycoprotein V2 region (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

RN [1]
RP SEQUENCE FROM N.A.
RA Wang B., Saksena N.K.;
RT "HIV-1 strains from a cohort of American subjects reveal the presence
of a V2 region extension unique to slow progressors and non-
progressors.";
RL AIDS 0:0-0(2000).
DR EMBL: AF203211; AAF24360.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 42 42
SQ SEQUENCE 42 AA; 4790 MW; DE78892C9F92A38B CRC64;

Query Match 100.0%; Score 20; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
Db 22 NLDA 25

RESULT 13

O8T643 PRELIMINARY; PRT; 50 AA.
AC O8T643;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Integrin betaps4A (Fragment).
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE FROM N.A.
RA Bunch T.A., Miller S.W., Brower D.L.;
RT "Mutations in the C8-C9 loop of the Drosophila betaps subunit affect
integrin regulation.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF487330; AAL93259.1; -.
FT NON_TER 1 1
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5436 MW; 610D4253BFFDF5C4 CRC64;

Query Match 100.0%; Score 20; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
Db 47 NLDA 50

RESULT 14

O8T642 PRELIMINARY; PRT; 50 AA.
AC O8T642;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Integrin betaps4B (Fragment).
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE FROM N.A.
RA Bunch T.A., Miller S.W., Brower D.L.;
RT "Mutations in the C8-C9 loop of the Drosophila betaps subunit affect
integrin regulation.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF487331; AAL93260.1; -.
FT NON_TER 1 1
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 5469 MW; C82D2269C7016957 CRC64;

Query Match 100.0%; Score 20; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
Db 47 NLDA 50

RESULT 15

O8RAW6

ID Q8RAM6 PRELIMINARY; PRT; 51 AA.
 AC Q8RAM6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein TTE1072.
 GN TTE1072.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4r / JCM11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.,
 RT "A complete sequence of T. tengcongensis genome."
 RL Genome Res. 12:689-700(2002).
 DR EMBL: AE013071; AAM24319.1;
 KW Hypothetical protein; Complete proteome
 SQ SEQUENCE 51 AA; 6136 MW; 9E96B9BF4F7993 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 12 NLDA 15

RESULT 16

ID Q99ZY5 PRELIMINARY; PRT; 54 AA.
 AC Q99ZY5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SpY1017.
 GN SpY1017.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 DR EMBL: AE006546; AAK33913.1;
 KW Hypothetical protein; Complete proteome
 SQ SEQUENCE 54 AA; 6433 MW; 5EDE5E737514DF91 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 54;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 20 NLDA 23

RESULT 17
 OY1TH0 PRELIMINARY; PRT; 57 AA.
 AC Q91TH0;
 ID Q91TH0;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE T126.
 OS Tupala herpesvirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae.
 OX NCBI_TaxID=10397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2;
 RX MEDLINE=21211637; PubMed=11312357;
 RA Bahr U., Darai G.,
 RT "Analysis and Characterization of the Complete Genome of Tupala (Tree
 Shrew) Herpesvirus."
 RL J. Virol. 75:4854-4870(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2;
 RX Darai G., Bahr U.,
 RT Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF281817; AAK57177.1;
 KW Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 SQ SEQUENCE 57 AA; 6165 MW; BD252F7AB2C724A4 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 53 NLDA 56

RESULT 18

ID Q96X11 PRELIMINARY; PRT; 66 AA.
 AC Q96X11;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Matrig type 2 protein (Fragment).
 OS Phaeosphaeria avenaria f. sp. triticae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC Dothideomycetes et Chaetothyriomycetes Incertae sedis;
 OC Phaeosphaeriaceae; Phaeosphaeria.
 OX NCBI_TaxID=54790;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC26370;
 RA Dai Q., Cui K., Ueng P.P.,
 RT "Matrig type gene in Phaeosphaeria avenaria f. sp. triticae."
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF358826; AAK51442.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR000910; HMG_12_box.
 DR Pfam: PF00505; HMG_box_1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 66 AA; 7936 MW; 532A84F37D334DBA CRC64;

Query Match 100.0%; Score 20; DB 3; Length 66;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 DB 35 NLDA 38

RESULT 19
 OY7XY3 PRELIMINARY; PRT; 68 AA.
 ID Q97XY3

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AC 09TX3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 7.7 kDa protein.
GN F46F5.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderae; Caenorhabditis.
OC NCBL_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=9069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Miller N., Mamsley P., Twyman B.;
RT "The sequence of C. elegans cosmid F46F5.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF106577; AAC78187.1; -.
KW Hypothetical protein.
SQ SEQUENCE 68 AA; 7672 MW; FB096444AC007693 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 5; Length 68;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 32 NLDA 35

RESULT 20
Q8VA17 PRELIMINARY; PRT; 69 AA.
AC Q8VA17;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Wsv425 (WSSV484).
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBL_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21548311; PubMed=11689662;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
RL J. Virol. 75:11811-11820(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RX MEDLINE=20517548; PubMed=11062040;
RA Tsai M.F., Yu H.T., Tzeng H.F., Lwu J.H., Chou C.M., Huang C.J.,
RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
RT "Identification and characterization of a shrimp white spot syndrome
RT virus (WSSV) gene that encodes a novel chimeric polypeptide of

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RT cellular-type thymidine kinase and thymidylate kinase.";
RL Virology 277:100-110(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RX MEDLINE=21548656; PubMed=11689058;
RA Liu W.J., Yu H.T., Peng S.E., Chang Y.S., Pien H.W., Lin C.J.,
RA Huang C.J., Tsai M.F., Huang C.D., Wang C.H., Lin J.Y., Lo C.F.,
RA Kou G.H.;
RT "Cloning, characterization, and phylogenetic analysis of a shrimp
RT white spot syndrome virus gene that encodes a protein kinase.";
RL Virology 289:362-377(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RX MEDLINE=21844071; PubMed=11853398;
RA Chen L.L., Lwu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
RA Lo C.F., Kou G.H.;
RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
RT spot syndrome virus and characterization of the motif important for
RT targeting VP35 to the nuclei of transfected insect cells.";
RL Virology 293:44-53(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RA Lo C.F., Kou G.H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332093; AAL33427.1; -.
DR EMBL; AF440570; AAL89352.1; -.
SQ SEQUENCE 69 AA; 7916 MW; 20754BFC9B673FF CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 12; Length 69;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 53 NLDA 56

RESULT 21
Q93PT2 PRELIMINARY; PRT; 71 AA.
AC Q93PT2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Glycerol-3-phosphate dehydrogenase (Fragment).
GN GPD.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBL_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21318691; PubMed=11425718;
RA Boels I.C., Ramos A., Kleerebezem M., de Vos W.M.;
RT "Functional Analysis of the Lactococcus lactis gatl and gatl genes and
RT their impact on sugar nucleotide and Exopolysaccharide Biosynthesis.";
RL Appl. Environ. Microbiol. 67:3033-3040(2001).
DR EMBL; AF304368; AAC71622.1; -.
DR InterPro; IPR001652; NAD_gly3p_dh.
DR Pfam; PF01210; NAD_gly3p_dh; 1.
FT NON_TER
SQ SEQUENCE 71 AA; 8135 MW; D06126B27C4BC8D5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 71;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 45 NLDA 48

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RESULT 22

099TW2 PRELIMINARY; PRT; 72 AA.
AC 099TW2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein SAV1532.
GN SAV1532 OR SA1532.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;

RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003362; BAB57694.1; -;
DR EMBL: AP003134; BAB42624.1; -;
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 72 AA; 8729 MW; 2C6891D3F9FD695 CRC64;

Query Match

Best Local Similarity 100.0%; Score 20; DB 16; Length 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 20 NLDA 23

RESULT 23

095641 PRELIMINARY; PRT; 73 AA.
AC 095641;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative zinc finger protein H140 (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RN Lee P.T., Gelbart T., West C., Adams M., Blackstone R.;
RT Identification of 15 genes mapping to a region of chromosome 6p21.3
RT encompassing the microsatellite markers D6S306 and D6S1260.
RT Characterization of 3 genes encoding zinc finger proteins.";
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U00232; AAD00353.1; -;
DR INTERPRO: IPR000822; Znf_C2H2.
DR PROSITE: PS01557; ZINC_FINGER_C2H2_2; 1.
KW DNA-binding; Zinc-finger.
FT NON_TER 1
FT NON_TER 73

Query Match 100.0%; Score 20; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 15 NLDA 18

RESULT 24

08X2G0 PRELIMINARY; PRT; 73 AA.
AC 08X2G0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Ecs1392.
GN Ecs1392.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;

RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Ikeda T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.,
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Rep. 8:11-22(2001).
DR EMBL: AP002554; BAB34815.1; -;
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8364 MW; 3F30F3233977E969 CRC64;

Query Match

Best Local Similarity 100.0%; Score 20; DB 16; Length 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLDA 4
DB 67 NLDA 70

RESULT 25

09PND7 PRELIMINARY; PRT; 75 AA.
AC 09PND7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Small hydrophobic protein.
GN CJI158C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;

RP SEQUENCE FROM N.A.
RN STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltham S.,
RA Jagers K., Karyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL: AL139077; CAB73412.1; -;
KW Complete proteome.

Query Match 100.0%; Score 20; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Query Match 100.0%; Score 20; DB 16; Length 75;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 6 NIDA 9

RESULT 26

ID 08XVB9 PRELIMINARY; PRT; 75 AA.
 AC 08XVB9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 GN RSC2912 OR R500183.
 DE Hypothetical protein RSC2912.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMT1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brotlier P., Camus J.C., Catolico L.,
 RA Chandler M., Choise N., Claudet-Renard C., Cunne S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiek T.,
 RA Siguler P., Thebault P., Boucher C.A.,
 RA Weissbach J., Whalen M., Wincker P., Levy M.,
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 KW EMBL: AF646072; CAD16619.1; -;
 DM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 75 AA; 8174 MM; 4F207ASB257FC58B CRC64;

Query Match 100.0%; Score 20; DB 16; Length 75;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 64 NIDA 67

RESULT 27

ID 08T640 PRELIMINARY; PRT; 80 AA.
 AC 08T640;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 GN Integrin betaps (Fragment).
 DE Integrin betaps (Honeybee).
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata;
 OC Apoidea; Apidae; Apis.
 OX NCBI_TaxID=7460;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Bunch T.A., Miller S.W., Brower D.L.;
 RT "Mutations in the C8-C9 loop of the drosophila betaps subunit affect
 integrin regulation";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF487333; AAL93262.1; -;
 FT NON_TER 1 1
 FT NON_TER 80 80
 SQ SEQUENCE 80 AA; 8766 MM; 64AFCE43C0DFC01A CRC64;

Query Match 100.0%; Score 20; DB 5; Length 80;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 54 NIDA 57

RESULT 28

ID 09AXX2 PRELIMINARY; PRT; 83 AA.
 AC 09AXX2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Beta 1,3 glucanase (Fragment).
 GN 1,3 GLUCAN-BN-1.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. DARMOR-BZH.
 RA Fournier M., Froger N., Brunel D.;
 RT "Amplified consensus gene markers: Tools designing for a genetic map
 of Arabidopsis known-function genes in Brassica";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF229403; AAK00675.1; -;
 DR HSP: P15737; IGHS.
 DR InterPro: IPR000490; Glyco_hydro_17.
 DR Pfam: PF00332; Glyco_hydro_17; 1.
 FT NON_TER 1 1
 FT NON_TER 83 83
 SQ SEQUENCE 83 AA; 9276 MM; 6BF6ACE39FC9BCC CRC64;

Query Match 100.0%; Score 20; DB 10; Length 83;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NIDA 4
 ||||
 Db 60 NIDA 63

RESULT 29

ID 09AXX0 PRELIMINARY; PRT; 85 AA.
 AC 09AXX0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Beta 1,3 glucanase (Fragment).
 GN 1,3 GLUCAN-BR-2.
 OS Brassica campestris (Field mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3711;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. R500;
 RA Fournier M., Froger N., Brunel D.;
 RT "Amplified consensus gene markers: Tools designing for a genetic map
 of Arabidopsis known-function genes in Brassica";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF229405; AAK00677.1; -;
 DR HSP: P15737; IGHS.
 DR InterPro: IPR000490; Glyco_hydro_17.
 DR Pfam: PF00332; Glyco_hydro_17; 1.
 FT NON_TER 1 1
 FT NON_TER 85 85
 SQ SEQUENCE 85 AA; 9436 MM; 10A5AF6342704506 CRC64;

Query Match 100.0%; Score 20; DB 10; Length 85;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 61 NLDA 64

RESULT 30
 ID Q8X6S5 PRELIMINARY; PRT; 85 AA.
 AC Q8X6S5;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE Glutaredoxin1 redox coenzyme for glutathione-dependent
 DE ribonucleotide reductase.
 GN GRXA OR Z1076 OR ECS0929.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postfist G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Groth C.E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocous K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 DR EMBL: AE005266; AAG5225.1; -;
 DR EMBL: AF002553; BAB34352.1; -;
 DR InterPro: IPR002109; Glutaredoxin.
 DR InterPro: IPR000063; Thiores.
 DR Pfam: PF00462; glutaredoxin; 1.
 DR PRINTS: PR00160; GLUTAREDOXIN; 1.
 DR PROSITE: PS00195; GLUTAREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 85 AA; 9695 MW; 8C3C15A473ED2041 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 85;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 82 NLDA 85

RESULT 31
 ID Q8T641 PRELIMINARY; PRT; 86 AA.
 AC Q8T641;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Integrin betaps (Fragment).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pelegrina; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylsia;
 OC Sphingidae; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bunch T.A., Miller S.W., Brower D.L.;
 RT "Mutations in the C8-C9 loop of the Drosophila betaps subunit affect
 RT integrin regulation.";
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF487332; AAL93261.1; -;
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 86 AA; 9488 MW; 6110C0042436FDA1 CRC64;

Query Match 100.0%; Score 20; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 56 NLDA 59

RESULT 32
 ID Q9X5H7 PRELIMINARY; PRT; 88 AA.
 AC Q9X5H7;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE HELA.
 GN HELA.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43504;
 RX MEDLINE=99214098; PubMed=10198012;
 RA McGee D.J., May C.A., Garner R.M., Himpel J.M., Mobley H.L.T.;
 RT "Isolation of Helicobacter pylori genes that modulate urease
 RT activity.";
 RL J. Bacteriol. 181:2477-2484(1999).
 DR EMBL: AF125214; AAD27694.1; -;
 SQ SEQUENCE 88 AA; 10190 MW; 6C301645517BD2E3 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 57 NLDA 60

RESULT 33
 ID Q9AKH6 PRELIMINARY; PRT; 89 AA.
 AC Q9AKH6;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 9.3 kDa protein.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=783;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=84-21C;
 RX MEDLINE=21219194; PubMed=11319266;
 RA Andersson J.O., Andersson S.G.E.;
 RT "Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";
 RL Mol. Biol. Evol. 18:829-839(2001).
 DR EMBL: AJ293320; CAC33684.1; -.
 KW Hypothetical protein.
 SO SEQUENCE 89 AA; 9331 MW; 8CF96A2C7AAB29A2 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 35 NLDA 38

RESULT 34
 092J16 PRELIMINARY; PRT; 89 AA.
 AC 092J16;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein RC0233.
 GN RC0233.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MALISH 7;
 RA MEDLINE=21442074; PubMed=11557893;
 RA Oyata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barde V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
 RL Science 293:2093-2098(2001).
 DR EMBL: AE008592; AL02791.1; -.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 89 AA; 9402 MW; ED502B6FC370ADB7 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 89;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 35 NLDA 38

RESULT 35
 09H4V4 PRELIMINARY; PRT; 91 AA.
 AC 09H4V4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DJ1187J4.2 (Novel protein similar to rat Rf3) (Fragment).
 GN DJ1187J4.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Bird C.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL355392; CAC15882.1; -.
 FT NON_TER 1
 SO SEQUENCE 91 AA; 9774 MW; F351A7560E7387BD CRC64;

Query Match 100.0%; Score 20; DB 4; Length 91;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 52 NLDA 55

RESULT 36
 007938 PRELIMINARY; PRT; 91 AA.
 ID 007938;
 AC 007938;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein yrdF.
 GN YRDF.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1A1;
 RA Belitsky B.R., Gustafsson M.C.U., Sonenshein A.L., von Wachenfeldt C.,
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
 RA Duesterhoeft A., Ehrlich S.D.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borstis R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings S.D., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Britan K.D., Errington J., Rabret C., Ferrari E., Foulger D.,
 RA Fritsch C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Chim S.T., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppt G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Meuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudga B., Park S.H.,
 RA Parro V., Pohl T.M., Portelle D., Portwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Repoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Rocha E., Roche B., Rose M., Sadie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scottone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Takakoshi A., Tanaka T., Terstra P., Toironi A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vanier F., Vassart A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
 RP [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11043; CAAT71938.1; -
 DR EMBL: U93875; AAB80899.1; -
 DR EMBL: Z99117; CAB14614.1; -
 DR HSP; P11540; 1820.
 DR InterPro: IPR000468; Barstar.
 DR Pfam: PF01337; Barstar.1.
 DR Prodom: PD029050; Barstar.1.
 KM Hypothetical protein, Complete proteome.
 SQ SEQUENCE 91 AA; 10728 MW; F001CB84888DA11B CRC64;

Query Match 100.0%; Score 20; DB 16; Length 91;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 34 NLDA 37

RESULT 37
 O97KS3 PRELIMINARY; PRT; 91 AA.
 AC O97KS3;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Barstar-like protein ribonuclease (barnase) inhibitor.
 GN CAC0844.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1488;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE-21359325; PubMed-1146286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Olu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007600; AAK78820.1; -
 DR InterPro: IPR000468; Barstar.
 DR Pfam: PF01337; Barstar.1.
 DR Prodom: PD029050; Barstar.1.
 KM Complete proteome.
 SQ SEQUENCE 91 AA; 10821 MW; ADA8022BC9FCB8E CRC64;

Query Match 100.0%; Score 20; DB 16; Length 91;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 34 NLDA 37

RESULT 38
 O9RS22 PRELIMINARY; PRT; 92 AA.
 AC O9RS22;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE SSBl6(GAL4(1-147))-SSBl6 transcriptional repressor component.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN (1)

RP SEQUENCE FROM N.A.
 RX MEDLINE-93288141; PubMed-8510759;
 RA Saha S., Brickman J.M., Lehming N., Ptashne M.;
 RT "New eukaryotic transcriptional repressors.";
 RL Nature 363:648-652(1993).
 SQ SEQUENCE 92 AA; 10059 MW; C2F01CE9D1B15245 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
 ||||
 DB 60 NLDA 63

RESULT 39
 O99H35 PRELIMINARY; PRT; 92 AA.
 AC O99H35;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Oref12 (Hypothetical 10.8 kDa protein).
 OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus,
 OS Helicoverpa armigera nucleopolyhedrovirus G4, and
 OS Helicoverpa armigera nuclear polyhedrosis virus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10468, 148363, 51313;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa zea single nucleocapsid nucleopolyhedrovirus;
 RA Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
 RA Presnail J.K., Herriman R., Dolan M., Tingey S., Hu Z.-H., Viak J.M.;
 RT "Genome sequence analysis of Helicoverpa zea single nucleocapsid
 RT nucleopolyhedrovirus.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RA Deng F., Chen X., Viak J.M., Arif B.M., Hu Z.;
 RT "Sequence analysis of the gp37 gene of Heliothis armigera single-
 RT nucleocapsid nucleopolyhedrovirus.";
 RL zhongguo Bingduxue 15:35-42(2000).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RA Wang H., Hu Z., Sun X., Viak J.M., Chen X.;
 RT "Sequence analysis of the jap3 gene of Heliothis armigera single-
 RT nucleocapsid nucleopolyhedrovirus.";
 RL zhongguo Bingduxue 15:43-49(2000).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RX MEDLINE-21078302; PubMed-11210934;
 RA Wang H., Chen X., Wang H., Arif B.M., Viak J.M., Hu Z.;
 RT "Nucleotide sequence and transcriptional analysis of a putative basic
 RT DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
 RL Virus Genes 22:113-120(2001).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RX MEDLINE-21064569; PubMed-11125177;
 RA Chen X., Iukel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
 RA Peters S., Zuidema D., Lankhorst R.K., Viak J.M., Hu Z.;
 RT "The sequence of the Helicoverpa armigera single-nucleocapsid
 RT nucleopolyhedrovirus genome.";
 RL J. Gen. Virol. 82:241-257(2001).
 RN (6)
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RA Chen X., Iukel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,

RA Peters S., Zuidema D., Lankhorst R.K., Viak J.M., Hu Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=CI;
RA Zhang C.X., Wu J.C.;
RT "genome structure and the p10 gene of the Helicoverpa armigera
nucleopolyhedrovirus.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 33:179-184(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=CI;
RA Zhang C.X., Jin W.R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334030; AAL56157.1; -;
DR EMBL; AF271059; AAG53755.1; -;
DR EMBL; AF303045; AAK96267.1; -;
DR InterPro: IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM_14; 1.
DR SMART; SM00494; ChtBD2; 1.
KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10780 MW; 9628054EDE3C4ED3 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 92;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 67 NLDA 70

RESULT 40
Q8ZAU6 PRELIMINARY; PRT; 93 AA.
ID Q8ZAU6;
AC Q8ZAU6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative ribonuclease inhibitor.
GN YPO3690.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
NC NCBL_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE-21470413; PubMed-11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
RA Prentice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Leavelle T., Hamlin N., Holroyd S., Jagsals K., Kariyev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; A0414158; CAC93158.1; -;
DR InterPro: IPR000468; Barstar.
DR Pfam; PF01337; Barstar; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 93 AA; 10739 MW; E71C2AC8A9936F7B CRC64;

Query Match 100.0%; Score 20; DB 16; Length 93;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 34 NLDA 37

RESULT 41
ID Q9K0G0 PRELIMINARY; PRT; 95 AA.
AC Q9K0G0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribonuclease inhibitor Barstar.
GN NMB0646.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NC NCBL_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE-20175755; PubMed-10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
RA Colton M.D., Utechtack T.R., Khouli H., Qin H., Yamathavan J.,
RA Gill J., Scariato V., Maignani V., Pizarro M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappapoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002419; AAF41067.1; -;
DR HSSP; P11540; 1B27.
DR TIGR; NMB0646; -;
DR InterPro: IPR000468; Barstar.
DR Pfam; PF01337; Barstar; 1.
DR ProDom; PD029050; Barstar; 1.
KW Complete proteome.
SQ SEQUENCE 95 AA; 11385 MW; D79ABA9C84DD77B3 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLDA 4
||||
DB 33 NLDA 36

RESULT 42
ID Q79692 PRELIMINARY; PRT; 96 AA.
AC Q79692;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome b (fragment).
GN CYTB.
OS Stigmatura napsensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Stigmatura.
NC NCBL_TaxID=83304;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99184959; PubMed-10082611;
RA Roy M.S., Torres-Mura J.C., Hertel F.;
RT "Molecular phylogeny and evolutionary history of the tit-tyrants
(Aves: Tyrannidae).";
RL Mol. Phylogenet. Evol. 11:67-76(1999).
CC -I- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -I- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -I- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL: AF067000; AAC64030.1; -.
 DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF00033; cytochrome_b_b6_1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 96 96
 SQ SEQUENCE 96 AA; 10930 MW; BB0CDAB5CB7B9FE7 CRC64;
 Query Match 100.0%; Score 20; DB 8; Length 96;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLDA 4
 Db 55 NLDA 58

RESULT 43
 ID Q9V9P1 PRELIMINARY; PRT; 97 AA.
 AC Q9V9P1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CG10834 protein.
 GN CG10834.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Reese M.G.,
 RA Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003782; AAF57245.1; -.
 DR FlyBase; FBgn0032972; CG10834.
 DR InterPro: IPR004942; Rob1_LC7.
 DR Pfam: PF03259; Rob1_LC7; 1.
 SQ SEQUENCE 97 AA; 10922 MW; A9BAFD9A5686F1A2 CRC64;
 Query Match 100.0%; Score 20; DB 5; Length 97;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLDA 4
 Db 60 NLDA 63

RESULT 44
 ID Q9R9X3 PRELIMINARY; PRT; 101 AA.
 AC Q9R9X3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mera (Fragment).
 GN MERA.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bruce K.D., Lilley A.K., Bailey M.J.;
 RT "mer sequences on plasmids.";
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF092066; AAD52702.1; -.
 DR HSSP: P11959; IPRD
 DR InterPro: IPR004099; pyr_redox_dim.
 DR Pfam: PF02852; pyr_redox_dim; 1.
 KW Plasmid.
 FT NON_TER 1 1
 FT NON_TER 101 101
 SQ SEQUENCE 101 AA; 10480 MW; AB1520C13621FF89 CRC64;
 Query Match 100.0%; Score 20; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NLDA 4
 Db 15 NLDA 18

RESULT 45
 ID O20641 PRELIMINARY; PRT; 102 AA.
 AC O20641;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome b (Fragment).
 GN CYTB.
 OS Anabas testudineus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neoptera; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Perciformes; Perciformes;
 OC Anabantoidae; Anabantidae; Anabas.
 OX NCBI_TaxID=64144;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN-TEST1;
RA Chan W.C., Lee P.G.;
RT "Systematics of southeast Asian snakeheads using molecular and
RT morphological data.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -I- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -I- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RISKE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL: AF012791; AAB81754.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00033; cytochrome_b_n; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11344 MW; F51A0FAEC31850A2 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 102;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIDA 4
Db 49 NIDA 52

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Search completed: February 6, 2003, 11:22:05
 Job time : 24.3333 secs